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OM protein - protein search, using sw model

Run on: October 27, 2004, 08:33:39 ; Search time 132 Seconds
(without alignments)
827.733 Million cell updates/sec

Title: US-09-867-570-2

Perfect score: 1763
Sequence: 1 MESKSSWVIRLGFSLMDSTI.....EGGGWLPQRTLISGRLRQ 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1763	100.0	337	11	US-09-867-570-2
2	1688	95.7	332	9	US-09-995-225-20
3	1688	95.7	332	10	US-09-995-225-20
4	1688	95.7	332	14	US-10-183-116-31
5	1688	95.7	332	14	US-10-225-567A-674
6	1688	95.7	332	15	US-10-072-012-529
7	1688	95.7	332	15	US-10-072-012-534
8	1688	95.5	332	14	US-10-401-397A-2
9	1683	95.5	332	14	US-10-292-798-1274
10	1683	95.5	332	15	US-10-072-012-530
11	1683	95.5	332	15	US-10-072-012-535
12	1663	94.3	332	15	US-10-391-074-2
13	1639	93.0	314	14	US-10-219-834-79

14	1557	88.3	302	14	US-10-237-467-10	Sequence 10, Appl
15	1415.5	80.3	1589	15	US-10-072-012-528	Sequence 528, App
16	1415.5	80.3	1589	15	US-10-072-012-532	Sequence 532, App
17	1383	78.4	322	14	US-10-183-116-16	Sequence 16, Appl
18	1383	78.4	322	14	US-10-079-384-4	Sequence 4, Appl
19	1383	78.4	322	14	US-10-017-161-1056	Sequence 1056, Ap
20	1383	78.4	322	14	US-10-240-998-4	Sequence 4, Appl
21	1383	78.4	322	14	US-10-321-807-20	Sequence 20, Appl
22	1383	78.4	322	14	US-10-237-467-12	Sequence 12, Appl
23	1383	78.4	322	14	US-10-292-798-898	Sequence 898, App
24	1383	78.4	322	15	US-10-016-248-81	Sequence 81, Appl
25	1383	78.4	322	15	US-10-072-012-172	Sequence 172, App
26	1383	78.4	322	15	US-10-072-012-527	Sequence 527, App
27	1383	78.4	322	15	US-10-072-012-531	Sequence 531, App
28	1383	78.4	322	15	US-10-343-650A-44	Sequence 44, Appl
29	1383	78.4	322	16	US-10-321-807-20	Sequence 20, Appl
30	1383	78.4	322	16	US-10-314-048A-20	Sequence 20, Appl
31	1367	77.5	322	9	US-09-995-225-18	Sequence 18, Appl
32	1367	77.5	322	10	US-09-995-225-18	Sequence 18, Appl
33	1367	77.5	322	14	US-10-183-116-33	Sequence 33, Appl
34	1367	77.5	322	14	US-10-225-567A-689	Sequence 689, App
35	1367	77.5	322	14	US-10-237-467-4	Sequence 4, Appl
36	1367	77.5	322	15	US-10-016-248-84	Sequence 84, Appl
37	1367	77.5	322	15	US-10-072-012-531	Sequence 531, App
38	1367	77.5	322	15	US-10-072-012-536	Sequence 536, App
39	1365	77.2	319	15	US-10-072-012-174	Sequence 174, App
40	1361	77.2	322	14	US-10-292-798-1042	Sequence 1042, Ap
41	1313.5	74.5	323	15	US-10-072-012-178	Sequence 178, App
42	1263	71.6	328	14	US-10-219-834-20	Sequence 20, Appl
43	1031.5	58.5	331	16	US-10-467-616-2	Sequence 2, Appl
44	989.5	56.1	330	9	US-09-826-508-12	Sequence 12, Appl
45	989.5	56.1	330	9	US-09-750-373-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-867-570-2
Sequence 2, Application US/09867570
Publication No. US20040076951A1
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USBS THEREOF
FILE REFERENCE: CL000900-CIP
CURRENT APPLICATION NUMBER: US/09/867,570
CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/695,045
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 337
TYPE: PRT
ORGANISM: Human
US-09-867-570-2

Query Match 100.0%; Score 1763; DB 11; Length 337;
Best Local Similarity 100.0%; Pred. No. 7; 4e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESKSSWVIRLGFSLMDSTIPVLTGELTPINGRETPCYKOTISFPTGLTCTIVSLVALTGN 60
DB 1 MESKSSWVIRLGFSLMDSTIPVLTGELTPINGRETPCYKOTISFPTGLTCTIVSLVALTGN 60
QY 61 AVLTWLTGMRBNRNVASYITLNVADPLFLSGHITCSPLRLINHPISKILSPWVTP 120
DB 61 AVLTWLTGMRBNRNVASYITLNVADPLFLSGHITCSPLRLINHPISKILSPWVTP 120
QY 121 YPTGLSMLSAISTERCLSTIPWYHCRPRRYSSVMCYLWALSILRSITLWMPDCPLF 180
DB 121 YPTGLSMLSAISTERCLSTIPWYHCRPRRYSSVMCYLWALSILRSITLWMPDCPLF 180

Db 121 YFGLSMLSAISTERCSTILMPWYHCRPRYLSSVMCVLLMALSLRSILEMFCDFLF 180
Qy 181 SGADSVWCETSDFTTIAVLVFLCVVLICGSSSLVLRILCGSRKMPLTRLYTTLITVLVF 240
Db 181 SGADSVWCETSDFTTIAVLVFLCVVLICGSSSLVLRILCGSRKMPLTRLYTTLITVLVF 240
Qy 241 LCGSPFGIOWALFSRHLDMKVLFCVHLVSLFSLNSSANPITYFVGSFRORONRQ 300
Db 241 LCGSPFGIOWALFSRHLDMKVLFCVHLVSLFSLNSSANPITYFVGSFRORONRQ 300
Qy 301 NLKVLQRALQDTPREVDEGGWMLPQETTELSSGRLEQ 337
Db 301 NLKVLQRALQDTPREVDEGGWMLPQETTELSSGRLEQ 337

RESULT 2

US-09-995-225-20
Sequence 20, Application US/09995225
Publication No. US20020193584A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Zhong Liang
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,365
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,032
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/290,917
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 322
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US20020193584A1 Sequence
US-09-995-225-20

Query Match 95.7%; Score 1688; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.6e-145;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MDSTIPVAGTETPLINGREETPCYKOTLSFTGLCTIVLVAALVAVVLLGCGMRRA 75
Db 1 MDSTIPVAGTETPLINGREETPCYKOTLSFTGLCTIVLVAALVAVVLLGCGMRRA 60
Qy 76 VSIYIILNVADFLFSGHIIICSPRLINIRHPISKILSPVWTFPYIGLSMLSAISTER 135

Db 61 VSIYIILNVADFLFSGHIIICSPRLINIRHPISKILSPVWTFPYIGLSMLSAISTER 120
Qy 136 CLSTIMPWYHCRPRYLSSVMCVLLMALSLRSILEMFCDFLFSGADSVWCETSDFT 195
Db 121 CLSTIMPWYHCRPRYLSSVMCVLLMALSLRSILEMFCDFLFSGADSVWCETSDFT 180
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Db 181 IAMLVFLCVVLICGSSSLVLRILCGSRKMPLTRLYTTLITVLVFLICGSPFGIOWALFS 240
Qy 256 RIHDMKVLFCVHLVSLFSLNSSANPITYFVGSFRORONRQNLKVLQRALQDTP 315
Db 241 RIHDMKVLFCVHLVSLFSLNSSANPITYFVGSFRORONRQNLKVLQRALQDTP 300
Qy 316 VDEGGWMLPQETTELSSGRLEQ 337
Db 301 VDEGGWMLPQETTELSSGRLEQ 322

RESULT 3

US-09-995-225-20
Sequence 20, Application US/09995225
Publication No. US20030139588A9
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,365
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,032
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/290,917
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 322
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US20030139588A9 Sequence
US-09-995-225-20

Query Match 95.7%; Score 1688; DB 10; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.6e-145;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELTPIINGRETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMLLGCRMRNA 75
DB 1 MDSTIPVLGTELTPIINGRETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMLLGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMISAISTER 135
DB 61 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMISAISTER 120
QY 136 CUSILMPPIWYHCRPRYLSGVCVLLMALSLRSILEMFCDFLPSGADSVWCETSDFTT 195
DB 121 CUSILMPPIWYHCRPRYLSGVCVLLMALSLRSILEMFCDFLPSGADSVWCETSDFTT 180
QY 196 IAMLVFLCVLCCSSVLVLRILCGSRKMPRLRYVTIILLTVLVFLCGLPFGIQWALFS 255
DB 181 IAMLVFLCVLCCSSVLVLRILCGSRKMPRLRYVTIILLTVLVFLCGLPFGIQWALFS 240
QY 256 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALADTPE 315
DB 241 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALADTPE 300
QY 316 VDEGGGMLPOETLELSGSRLEQ 337
DB 301 VDEGGGMLPOETLELSGSRLEQ 322

RESULT 4

US-10-183-116-31
; Sequence 31, Application US/10183116
; Publication No. US2003092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Kinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-Kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE, 4CICPI
; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-183-116-31

Query Match 95.7%; Score 1688; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 4,6e-145;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELTPIINGRETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMLLGCRMRNA 75
DB 1 MDSTIPVLGTELTPIINGRETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMLLGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMISAISTER 135
DB 61 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMISAISTER 120
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QY 196 IAMLVFLCVLCCSSVLVLRILCGSRKMPRLRYVTIILLTVLVFLCGLPFGIQWALFS 255
DB 181 IAMLVFLCVLCCSSVLVLRILCGSRKMPRLRYVTIILLTVLVFLCGLPFGIQWALFS 240
QY 256 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALADTPE 315
DB 241 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALADTPE 300
QY 316 VDEGGGMLPOETLELSGSRLEQ 337
DB 301 VDEGGGMLPOETLELSGSRLEQ 322

RESULT 5

US-10-225-567A-674
; Sequence 674, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Rouse, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 674
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-674

Query Match 95.7%; Score 1688; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 4,6e-145;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDSTIPVLGTELTPIINGRETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMLLGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMISAISTER 135
DB 61 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFGLSMISAISTER 120
QY 136 CUSILMPPIWYHCRPRYLSGVCVLLMALSLRSILEMFCDFLPSGADSVWCETSDFTT 195
DB 121 CUSILMPPIWYHCRPRYLSGVCVLLMALSLRSILEMFCDFLPSGADSVWCETSDFTT 180
QY 196 IAMLVFLCVLCCSSVLVLRILCGSRKMPRLRYVTIILLTVLVFLCGLPFGIQWALFS 255
DB 181 IAMLVFLCVLCCSSVLVLRILCGSRKMPRLRYVTIILLTVLVFLCGLPFGIQWALFS 240
QY 256 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALADTPE 315
DB 241 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALADTPE 300
QY 316 VDEGGGMLPOETLELSGSRLEQ 337
DB 301 VDEGGGMLPOETLELSGSRLEQ 322

RESULT 6

US-10-072-012-529
; Sequence 529, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan

```

/ APPLICANT: Paturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsebrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ PRIOR APPLICATION NUMBER: 60/267,459
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 529
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-529

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Query Match          95.7%; Score 1688; DB 15; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.6e-145;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 16 MDSTIPVAGTELTPTINGREPTCYKQTSFTGLCTIVSLVLTGNAVVLMLGCMRANA 75
DB 1 MDSTIPVAGTELTPTINGREPTCYKQTSFTGLCTIVSLVLTGNAVVLMLGCMRANA 60
QY 76 VSIYIILNVAADFLPLSGHII CSPRLINIRHPISKILSPVTPFPYFGLSMLAISTER 135
DB 61 VSIYIILNVAADFLPLSGHII CSPRLINIRHPISKILSPVTPFPYFGLSMLAISTER 120
QY 136 CLSTIWPPIWTHCRPRYSVWCVLMLALSLRSLILEMFCDFLPSGADSWCETSDPTT 195
DB 121 CLSTIWPPIWTHCRPRYSVWCVLMLALSLRSLILEMFCDFLPSGADSWCETSDPTT 180
QY 196 IAWIPLCVVLGSGSLVLLVRLILGSRKMPILTRIVTTLITVLLVLLGLPFGIOMALFS 255
DB 181 IAWIPLCVVLGSGSLVLLVRLILGSRKMPILTRIVTTLITVLLVLLGLPFGIOMALFS 240

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QY 256 RIHDMKYLFCFHVHLSIFLSALNSSANPITTFPVGSFRORORONLKVLRALODTPE 315
DB 241 RIHDMKYLFCFHVHLSIFLSALNSSANPITTFPVGSFRORORONLKVLRALODTPE 300
QY 316 VDEGGWLPORTELSSGRLEQ 337
DB 301 VDEGGWLPORTELSSGRLEQ 322

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RESULT 7

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US-10-072-012-534
/ Sequence 534, Application US/10072012
/ Publication No. US2004003493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsebrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 534
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-534

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Query Match          95.7%; Score 1688; DB 15; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.6e-145;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

/ APPLICANT: Raetelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsbrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 530
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-072-012-530

Query Match          95.5%; Score 1683; DB 15; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.3e-144;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSITPVLTGTELTPIINGREETPCYKQTLSFTGLCTIVSLVATLGNAAVVMILGCRMRNA 75
DB 1 MDSITPVLTGTELTPIINGREETPCYKQTLSFTGLCTIVSLVATLGNAAVVMILGCRMRNA 60
QY 76 VSIYILNVADPLFLSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
DB 61 VSIYILNVADPLFLSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 120
QY 136 CLSTLMPITWYHCRPRRYLSSVWCVLMLSLRSLILEMWFCDPLFSGANSWCETSDPT 195
DB 121 CLSTLMPITWYHCRPRRYLSSVWCVLMLSLRSLILEMWFCDPLFSGANSWCETSDPT 180
QY 196 IAMVLPFCVVLGSSSLVLLVRLGSRKMPLTRLVTTIILTVLVEFLGCLPGIOMALFS 255
DB 181 IAMVLPFCVVLGSSSLVLLVRLGSRKMPLTRLVTTIILTVLVEFLGCLPGIOMALFS 240
QY 256 RIHLDMKVLFCGHVLSIFLSALNSSANPIIYFVGSFRORONRNLKVLQRALQDTP 315
DB 241 RIHLDMKVLFCGHVLSIFLSALNSSANPIIYFVGSFRORONRNLKVLQRALQDTP 300
QY 316 VDEGGWLPQRTLELSSRL 337
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DB 301 VDEGGWLPQRTLELSSRL 322

RESULT 11
US-10-072-012-535
/ Sequence 535, Application US/10072012
/ Publication No. US2004003493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangoli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Raetelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsbrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 535
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-072-012-535

Query Match          95.5%; Score 1683; DB 15; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.3e-144;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSITPVLTGTELTPIINGREETPCYKQTLSFTGLCTIVSLVATLGNAAVVMILGCRMRNA 75
DB 1 MDSITPVLTGTELTPIINGREETPCYKQTLSFTGLCTIVSLVATLGNAAVVMILGCRMRNA 60
QY 76 VSIYILNVADPLFLSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
|||||
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Db 61 VSIIYIINLVAADEPLFSGHICSPRLINIRHPIISKILSPVMTFPYFGLSMLSAISTER 120
QY 136 CUSTLMPWYHCRPRYLSSVWCVLMLALSILSLEMFCDFLFGSADSVWCETSDPIT 195
Db 121 CUSTLMPWYHCRPRYLSSVWCVLMLALSILSLEMFCDFLFGSADSVWCETSDPIT 180
QY 196 IAWLVFLCVLCCSSVLVLRILCGSRKMPLTRLYVTITLTVAVPLLCGLPGIOWALFS 255
Db 181 IAWLVFLCVLCCSSVLVLRILCGSRKMPLTRLYVTITLTVAVPLLCGLPGIOWALFS 240
QY 256 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQALQDTPR 315
Db 241 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQALQDTPR 300
QY 316 VDEGGGMLPOETLELSGSRLEQ 337
Db 301 VDEGGGMLPOETLELSGSRLEQ 322

RESULT 12
US-10-391-074-2

/ Sequence 2, Application US/10391074
/ Publication No. US20040038345A1
/ GENERAL INFORMATION:
/ APPLICANT: Nehls, Michael
/ APPLICANT: Matlier, Frank
/ TITLE OF INVENTION: No. US20040038345A1 Human Seven-Transmembrane Receptors
/ FILE REFERENCE: 7705.0008-00-000
/ CURRENT APPLICATION NUMBER: US/10/391.074
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-391-074-2

Query Match 94.3%; Score 1663; DB 15; Length 322;
Best Local Similarity 99.4%; Pred. No. 8.5e-143;

Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELPIINGRETEPCYKOTLSFTGLCTIVSVALTGNNAVLMILGCRMRNA 75
Db 1 MDSTIPVLGTELPIINGRETEPCYKOTLSFTGLCTIVSVALTGNNAVLMILGCRMRNA 60
QY 76 VSIIYIINLVAADEPLFSGHICSPRLINIRHPIISKILSPVMTFPYFGLSMLSAISTER 135
Db 61 VSIIYIINLVAADEPLFSGHICSPRLINIRHPIISKILSPVMTFPYFGLSMLSAISTER 120
QY 136 CUSTLMPWYHCRPRYLSSVWCVLMLALSILSLEMFCDFLFGSADSVWCETSDPIT 195
Db 121 CUSTLMPWYHCRPRYLSSVWCVLMLALSILSLEMFCDFLFGSADSVWCETSDPIT 180
QY 196 IAWLVFLCVLCCSSVLVLRILCGSRKMPLTRLYVTITLTVAVPLLCGLPGIOWALFS 255
Db 181 IAWLVFLCVLCCSSVLVLRILCGSRKMPLTRLYVTITLTVAVPLLCGLPGIOWALFS 240
QY 256 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQALQDTPR 315
Db 241 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQALQDTPR 300
QY 316 VDEGGGMLPOETLELSGSRLEQ 337
Db 301 VDEGGGMLPOETLELSGSRLEQ 322

RESULT 13

US-10-219-834-79
/ Sequence 79, Application US/10219834
/ Publication No. US20030096751A1
/ GENERAL INFORMATION:

/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THEREIN
/ FILE REFERENCE: D0191 NP
/ CURRENT APPLICATION NUMBER: US/10/219.834
/ PRIOR FILING DATE: 2002-08-15
/ PRIOR APPLICATION NUMBER: US 60/313,658
/ PRIOR FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: US 60/340,703
/ PRIOR FILING DATE: 2001-10-30
/ PRIOR APPLICATION NUMBER: US 60/318,675
/ PRIOR FILING DATE: 2001-09-12
/ PRIOR APPLICATION NUMBER: US 60/355,596
/ PRIOR FILING DATE: 2002-02-06
/ PRIOR APPLICATION NUMBER: US 60/333,417
/ PRIOR FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: US 60/338,367
/ PRIOR FILING DATE: 2001-12-06
/ NUMBER OF SEQ ID NOS: 192
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 79
/ LENGTH: 314
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-219-834-79

Query Match 93.0%; Score 1639; DB 14; Length 314;
Best Local Similarity 97.5%; Pred. No. 1.3e-140;

Matches 314; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 16 MDSTIPVLGTELPIINGRETEPCYKOTLSFTGLCTIVSVALTGNNAVLMILGCRMRNA 75
Db 1 MDSTIPVLGTELPIINGRETEPCYKOTLSFTGLCTIVSVALTGNNAVLMILGCRMRNA 60
QY 76 VSIIYIINLVAADEPLFSGHICSPRLINIRHPIISKILSPVMTFPYFGLSMLSAISTER 135
Db 61 VSIIYIINLVAADEPLFSGHICSPRLINIRHPIISKILSPVMTFPYFGLSMLSAISTER 120
QY 136 CUSTLMPWYHCRPRYLSSVWCVLMLALSILSLEMFCDFLFGSADSVWCETSDPIT 195
Db 121 CUSTLMPWYHCRPRYLSSVWCVLMLALSILSLEMFCDFLFGSADSVWCETSDPIT 180
QY 196 IAWLVFLCVLCCSSVLVLRILCGSRKMPLTRLYVTITLTVAVPLLCGLPGIOWALFS 255
Db 181 IAWLVFLCVLCCSSVLVLRILCGSRKMPLTRLYVTITLTVAVPLLCGLPGIOWALFS 240
QY 256 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQALQDTPR 315
Db 241 RIHLDMKVLFCVHVLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQALQDTPR 300
QY 316 VDEGGGMLPOETLELSGSRLEQ 337
Db 293 VDEGGGMLPOETLELSGSRLEQ 314

RESULT 14

US-10-237-467-10
/ Sequence 10, Application US/10237467
/ Publication No. US20030186324A1
/ GENERAL INFORMATION:
/ APPLICANT: Liao, Jiaxu
/ APPLICANT: Gray, Nathanael S.
/ APPLICANT: Caldwell, Jeremy C.
/ APPLICANT: Schultz, Peter G.
/ APPLICANT: IRM LLC
/ TITLE OF INVENTION: Sensory Neuron Receptors
/ FILE REFERENCE: 021288-001300US
/ CURRENT APPLICATION NUMBER: US/10/237.467
/ PRIOR FILING DATE: 2003-01-14
/ PRIOR APPLICATION NUMBER: US 60/317,879
/ PRIOR FILING DATE: 2001-09-07
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10

LENGTH: 302
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
 OTHER INFORMATION: 7 (DNG7) (NT009307)
 US-10-237-467-10

Query Match 88.3%; Score 1557; DB 14; Length 302;
 Best Local Similarity 93.5%; Pred. No. 3.4e-133;
 Matches 301; Conservative 1; Mismatches 0; Indels 20; Gaps 1;

QY 16 MDSTIPVLGTELPINGREETPCYKQTLSPFGTLCIVSLVATGNVAVMLGCMRRNA 75
 DB 1 MDSTIPVLGTELPINGREETPCYKQTLSPFGTLCIVSLVATGNVAVMLGCMRRNA 40
 QY 76 VSTIILNVADPFLSGHIIICSPRLINIRHPISKILSPWTFEYFGLSLAISTER 135
 DB 41 VSTIILNVADPFLSGHIIICSPRLINIRHPISKILSPWTFEYFGLSLAISTER 100
 QY 136 CLSTLWPIWHCRPRVLSVWCVLLMALSLRLSILEMFCDFLFGSADSVWCETSDFT 195
 DB 101 CLSTLWPIWHCRPRVLSVWCVLLMALSLRLSILEMFCDFLFGSADSVWCETSDFT 160
 QY 196 IAWTVFLCVLCGSSVLVLRILCGSRKMPRLTYVTLVTLVLLCGLPFGIOMAFS 255
 DB 161 IAWTVFLCVLCGSSVLVLRILCGSRKMPRLTYVTLVTLVLLCGLPFGIOMAFS 220
 QY 256 RIHDMKVLPCGHVLSIFLSALNSSANPIIYFVGSPRORONKLVORALODPE 315
 DB 221 RIHDMKVLPCGHVLSIFLSALNSSANPIIYFVGSPRORONKLVORALODPE 280
 QY 316 VDEGGWLPQETLELSGSRLQ 337
 DB 281 VDEGGWLPQETLELSGSRLQ 302

RESULT 15
 US-10-072-012-528
 ; Sequence 528, Application US/10072012
 ; Publication No. US20040033493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tchervet, Velizar
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Zernhusen, Bryan
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Shinkets, Richard
 ; APPLICANT: Li, Li
 ; APPLICANT: Gangoli, Bsha
 ; APPLICANT: Padigan, Muralidhara
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Taupier Jr, Raymond J.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Coleman, Steven D.
 ; APPLICANT: Wolenc, Adam R.
 ; APPLICANT: Pena, Carol E. A
 ; APPLICANT: Furtak, Katarzyna
 ; APPLICANT: Grose, William M.
 ; APPLICANT: Alsbrook II, John P.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Burgess, Catherine E.
 ; TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-258
 ; CURRENT APPLICATION NUMBER: US/10/072,012
 ; CURRENT FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,102
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 60/265,514
 ; PRIOR FILING DATE: 2001-01-31

;; PRIOR APPLICATION NUMBER: 60/265,517
 ;; PRIOR FILING DATE: 2001-01-31
 ;; PRIOR APPLICATION NUMBER: 60/265,412
 ;; PRIOR FILING DATE: 2001-01-31
 ;; PRIOR APPLICATION NUMBER: 60/265,395
 ;; PRIOR FILING DATE: 2001-01-31
 ;; PRIOR APPLICATION NUMBER: 60/266,406
 ;; PRIOR FILING DATE: 2001-02-02
 ;; PRIOR APPLICATION NUMBER: 60/266,767
 ;; PRIOR FILING DATE: 2001-02-05
 ;; PRIOR APPLICATION NUMBER: 60/267,057
 ;; PRIOR FILING DATE: 2001-02-07
 ;; PRIOR APPLICATION NUMBER: 60/266,975
 ;; PRIOR FILING DATE: 2001-02-07
 ;; PRIOR APPLICATION NUMBER: 60/267,459
 ;; PRIOR FILING DATE: 2001-02-08
 ;; Remaining Prior Application data removed - See File Wrapper or PALM.
 ;; NUMBER OF SEQ ID NOS: 1391
 ;; SOFTWARE: Patent Ver. 2.1
 ;; SEQ ID NO 528
 ;; LENGTH: 1589
 ;; TYPE: PRT
 ;; ORGANISM: Homo sapiens
 US-10-072-012-528

Query Match 80.3%; Score 1415.5; DB 15; Length 1589;
 Best Local Similarity 79.7%; Pred. No. 1.5e-119;
 Matches 279; Conservative 16; Mismatches 38; Indels 17; Gaps 1;

QY 5 SSW-----VIRLGLSMDSTIPVLGTELPINGREETPCYKQTLSPFG 47
 DB 633 SSWHIKEHNAAGHGVSRKVRTRGLFSLMDPTLTSTLTPINGREETPCYKQTLSP 692
 QY 48 LTCIVSLVATGNVAVMLGCMRRNAVSIIYIINLVADPFLSGHIIICSPRLINIRH 107
 DB 693 LTCIVSLVATGNVAVMLGCMRRNAVSIIYIINLVADPFLSGHIIICSPRLINIRH 752
 QY 108 PISKILSPWTFEYFGLSLAISTERCLSIIMPVTHCRPRVLSVWCVLLMALSLI 167
 DB 753 TISKILYFVMMFSYFAGISFLSAVSTERCLSVMPVYRCHRPVTHLSAVVCVLLMALSLI 812
 QY 168 RSTLEMMFCDFLFGSADSVWCETSDFTIIMVFLCVLCGSSVLVLRILCGSRKMP 227
 DB 813 RSTLEMMFCDFLFGSADSVWCETSDFTIIMVFLCVLCGSSVLVLRILCGSRKMP 872
 QY 228 RLVTYIILTVLFLCGLPFGIOMAFSRILDMKVLPCGHVLSIFLSALNSSANPIIY 287
 DB 873 RLVTYIILTVLFLCGLPFGIOMAFSRILDMKVLPCGHVLSIFLSALNSSANPIIY 932
 QY 288 FVGSPRORONKLVORALODPEVDEGGWLPQETLELSGSRLQ 337
 DB 933 FVGSPRORONKLVORALODPEVDEGGWLPQETLELSGSRLQ 982

Search completed: October 27, 2004, 08:45:33
 Job time : 133 secs

/note= "Casein kinase II (CK2) phosphorylation site"

FT XX WO200234914-A1.
 XX XX 02-MAY-2002.
 XX XX 10-OCT-2001; 2001WO-US031592.
 XX XX 25-OCT-2000; 2000US-00695045.
 PR 31-MAY-2001; 2001US-00867570.
 XX XX (PERKE) PE CORP NY.
 XX XX Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM;
 PI WPI; 2002-463360/49.
 DR N-PSDB; ABK52822, ABK52823.
 XX XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterized by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies.
 XX XX Claim 1; Fig 2; 75pp; English.

XX XX The present invention relates to a new G-protein coupled receptor (GPCR)
 CC peptide. The invention is useful for identifying a modulator of GPCR and
 CC for treating a disease or condition mediated by a human protease. The
 CC invention is also useful as models for the development of human
 CC therapeutics, for identifying therapeutic proteins, as targets for
 CC development of human therapeutic agents, and as query sequence to perform
 CC a search against sequence databases to, for e.g., identify other family
 CC members of related sequences. The vector of the invention is useful for
 CC producing a GPCR protein or peptide, for conducting cell-based assays
 CC involving the GPCR protein or its fragment, for identifying GPCR protein
 CC mutants whose functions are affected, and to produce non-human transgenic
 CC animals. The present amino acid sequence represents the human G-protein
 CC coupled receptor (GPCR) protein of the invention. This sequence is
 CC encoded by the human G-protein coupled receptor (GPCR) gene located on
 CC chromosome 3
 XX XX

SQ Sequence 337 AA;

Query Match 100.0%; Score 1763; DB 5; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.1e-180;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESKSSWTRIGFLSMDSTIPVLGTELPINRERTPCYKQTLSTFGLTCTISVALTGN 60
 DB 1 MESKSSWTRIGFLSMDSTIPVLGTELPINRERTPCYKQTLSTFGLTCTISVALTGN 60
 QY 61 AVVLMILGCRMRNNAVSIYILNVAADFLFSGHITCSPLRLINRHPISKILSPVMP 120
 DB 61 AVVLMILGCRMRNNAVSIYILNVAADFLFSGHITCSPLRLINRHPISKILSPVMP 120
 QY 121 YFGLSMLSAISTERCISILWPIWYHCRPRYLSSVMCVLWALSILRSILEMFCDFLF 180
 DB 121 YFGLSMLSAISTERCISILWPIWYHCRPRYLSSVMCVLWALSILRSILEMFCDFLF 180
 QY 181 SGASVWCETSDFTIAMLVFLCVLGGSSVLVRLICGSRKMPLTRLYTITLVVLF 240
 DB 181 SGASVWCETSDFTIAMLVFLCVLGGSSVLVRLICGSRKMPLTRLYTITLVVLF 240
 QY 241 LILGILPFIQWALFSRIHLDKVLFCVHVLVSIIFLSALNSSANPIIYFVGSFRORONQ 300
 DB 241 LILGILPFIQWALFSRIHLDKVLFCVHVLVSIIFLSALNSSANPIIYFVGSFRORONQ 300
 QY 301 NLKIVLQRALODTPEVDEGGGWLPOETTELSSRLLEQ 337
 DB 301 NLKIVLQRALODTPEVDEGGGWLPOETTELSSRLLEQ 337

RESULT 2

AA90761
 ID AA90761 standard; protein; 322 AA.
 XX XX

AC AA90761;
 XX XX
 DT 18-AUG-2000 (first entry)
 XX XX

DE Human G protein-coupled receptor hH17T213 SEQ ID NO:1.
 XX XX

KW Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
 XX XX genetic disease; cellular function regulation.
 KW XX

OS Homo sapiens.
 XX XX

PN WO20020455-A1.
 XX XX

PD 13-APR-2000.
 XX XX

PF 30-SEP-1999; 99WO-JP005366.
 XX XX

PR 01-OCT-1998; 98JP-00279535.
 XX XX

PA (TAKA) TAKEDA CHEM IND LTD.
 XX XX

PI Watanabe T, Terao Y, Matsui H;
 XX XX

DR WPI; 2000-303747/26.
 XX XX

DR N-PSDB; AAA29811.
 XX XX

PT Human-derived G protein-coupled protein and encoding nucleic acid, useful
 PT e.g. in determining ligands and treatment of diseases associated with
 PT dysfunction of the protein.
 XX XX

PS Claim 1; Page 90-91; 97pp; Japanese.
 XX XX

CC The present sequence represents a human-derived G protein-coupled protein
 CC designated hH17T213, which is isolated from the human hippocampus. The G
 CC protein-coupled receptor can be used for preventing, treating and
 CC diagnosing genetic diseases associated with G protein-coupled protein,
 CC and for regulating cellular functions. The protein can be used to prevent
 CC and treat disorders associated with G protein-coupled protein gene
 CC dysfunction. It can also be used to identify G protein-coupled protein
 CC ligands and generating antibodies and antisera against the protein. It is
 CC also useful in constructing recombinant receptor protein expression
 CC systems, developing receptor-binding assay systems and screening drug
 CC candidates, and can be used as a probe in the genetic diagnosis of G
 CC protein-coupled protein disorders
 XX XX

SQ Sequence 322 AA;

Query Match 95.7%; Score 1689; DB 3; Length 322;
 Best Local Similarity 100.0%; Pred. No. 1.2e-172;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVIGTILTPINGREETPCYKQTLSTFGLTCTISVALTGNNAVLMILGCRMRNA 75
 DB 1 MDSTIPVIGTILTPINGREETPCYKQTLSTFGLTCTISVALTGNNAVLMILGCRMRNA 60
 QY 76 VSIYILNVAADFLFSGHITCSPLRLINRHPISKILSPVMPPTPIGSMLSAISTER 135
 DB 76 VSIYILNVAADFLFSGHITCSPLRLINRHPISKILSPVMPPTPIGSMLSAISTER 120
 QY 136 CLSILMPIMYHCRPRYLSSVMCVLWALSILRSILEMFCDFLFGASVWCETSDFTI 195
 DB 136 CLSILMPIMYHCRPRYLSSVMCVLWALSILRSILEMFCDFLFGASVWCETSDFTI 180
 QY 196 IAMLVFLCVTGGSSVLVRLICGSRKMPLTRLYTITLVVFLCGIPFIQWALFS 255
 DB 196 IAMLVFLCVTGGSSVLVRLICGSRKMPLTRLYTITLVVFLCGIPFIQWALFS 240
 QY 256 RIHLDKVLFCVHVLVSIIFLSALNSSANPIIYFVGSFRORONKVLQRALODTPE 315
 DB 241 RIHLDKVLFCVHVLVSIIFLSALNSSANPIIYFVGSFRORONKVLQRALODTPE 300

Qy 316 VDEGGWLPQETLELSGSRLQ 337
 |||||
 Db 301 VDEGGWLPQETLELSGSRLQ 322

RESULT 3

ABJ04077
 ID ABJ04077 standard; protein; 322 AA.

AC ABJ04077;

DT 11-OCT-2002 (first entry)

DE Human G protein coupled receptor hrUP37.

KM Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31;
 hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37.

OS Homo sapiens.

PN WO200242461-A2.

PD 30-MAY-2002.

PF 26-NOV-2001; 2001WO-US044386.

PR 27-NOV-2000; 2000US-0253404P.

PR 12-DEC-2000; 2000US-0253366P.

PR 20-FEB-2001; 2001US-0270266P.

PR 20-FEB-2001; 2001US-0270266P.

PR 06-APR-2001; 2001US-0282032P.

PR 06-APR-2001; 2001US-0282356P.

PR 06-APR-2001; 2001US-0282356P.

PR 14-MAY-2001; 2001US-0290917P.

PR 31-JUL-2001; 2001US-0309208P.

XX (AREN-) ARENA PHARM INC.

PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;

XX WPI; 2002-566565/60.

DR N-PSDB; ABT04875.

XX Novel endogenous and non-endogenous versions of G protein-coupled

PT receptor useful for identification of candidate compounds as receptor

PT agonists or antagonists for use as therapeutic agents.

PS Claim 37; Page 75-76; 84pp; English.

XX The present invention provides the protein and coding sequences of

CC several human G-protein coupled receptors (GPCRs). These can be used in

CC the identification of candidate compounds as receptor agonists or inverse

CC agonists having applicability as therapeutic agents. The present sequence

CC is a GPCR protein of the invention

XX Sequence 322 AA;

Qy Query Match 95.7%; Score 1688; DB 5; Length 322;

Best Local Similarity 100.0%; Pred. No. 1.2e-172;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 MDSTIPVLTGTELPINGREBETPCYKOTLSFTGLTCTIVSLVATGNNAVVMMLGCRMRNA 75

Qy 1 MDSTIPVLTGTELPINGREBETPCYKOTLSFTGLTCTIVSLVATGNNAVVMMLGCRMRNA 60

Db 76 VSYIYIINLVADFLFSGHIIICSPRLINIRHPISTKLSVMTFPPYIGLSMISATSTER 135

Qy 61 VSYIYIINLVADFLFSGHIIICSPRLINIRHPISTKLSVMTFPPYIGLSMISATSTER 120

Db 136 CLSILWPIWYHCRPRYLSVVCVLLWALSILNLSIEMWCDPLFSGADSVWCETSDPT 195

Db 121 CLSILWPIWYHCRPRYLSVVCVLLWALSILNLSIEMWCDPLFSGADSVWCETSDPT 180
 Qy 196 IAWLVFLCVVLCGSSLVLRITICGRKMPFLRYVTITLVLPFLCGLPFGIOMALPS 255
 |||||
 Db 181 IAWLVFLCVVLCGSSLVLRITICGRKMPFLRYVTITLVLPFLCGLPFGIOMALPS 240
 Qy 256 RIHLDWKVLFCHVHVLVSIFLSALNNSANDPIYFVGSFRORONRNLKVLGRALQDTP 315
 |||||
 Db 241 RIHLDWKVLFCHVHVLVSIFLSALNNSANDPIYFVGSFRORONRNLKVLGRALQDTP 300
 Qy 316 VDEGGWLPQETLELSGSRLQ 337
 |||||
 Db 301 VDEGGWLPQETLELSGSRLQ 322

RESULT 4

AAE21296
 ID AAE21296 standard; protein; 322 AA.

AC AAE21296;

DT 01-JUL-2002 (first entry)

DE Human MrgX3 (mas-related gene) protein.

KM Human; mas-related gene; G-protein coupled receptor; drg-12 protein;
 receptor; sensory perception; pain; analgesic; MrgX3.

OS Homo sapiens.

PN WO200183555-A2.

PD 08-NOV-2001.

PF 04-MAY-2001; 2001WO-US014519.

PR 04-MAY-2000; 2000US-0202027P.

PR 01-AUG-2000; 2000US-0222344P.

PR 03-NOV-2000; 2000US-00704707.

PR 19-APR-2001; 2001US-0285493P.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

PI Anderson DJ, Dong X, Zylka M, Han S, Simon M;

XX WPI; 2002-171346/22.

DR N-PSDB; AAD33751.

XX Isolated polypeptide, Mrg, which is a G-protein coupled receptor and an

PT isolated polypeptide, drg-12, which is also a receptor, useful for

PT identifying agonists or antagonists for treating pain.

PS Claim 16; Page 130; 185pp; English.

XX The invention relates to Mrg (mas-related gene) protein, which is a G-

CC protein coupled receptor and drg-12 protein, which is a receptor. The

CC invention is useful for identifying compounds that bind to it, especially

CC agonists or antagonists. Administration of an agent (e.g. the identified

CC agonist) that increases the expression of Mrg in a mammal may be used for

CC treating impaired sensory perception in a mammal, especially pain. The

CC antagonist may also be useful for treating impaired sensory perception in

CC a mammal. The present sequence is human MrgX3 protein

XX Sequence 322 AA;

Qy Query Match 95.7%; Score 1688; DB 5; Length 322;

Best Local Similarity 100.0%; Pred. No. 1.2e-172;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 MDSTIPVLTGTELPINGREBETPCYKOTLSFTGLTCTIVSLVATGNNAVVMMLGCRMRNA 75

Qy 1 MDSTIPVLTGTELPINGREBETPCYKOTLSFTGLTCTIVSLVATGNNAVVMMLGCRMRNA 60

QY 76 VSIYILNVAAFLFLSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 135
Db 61 VSIYILNVAAFLFLSGHIIICSPRLINIRHPISKILSPVMTFFYFGLSMLSAISTER 120
QY 136 CLSLIMPTWYHCRRRYRSLSSVWCYLIMALSRLSILEMFCPLFGSGADSVWCERSDFTT 195
Db 121 CLSLIMPTWYHCRRRYRSLSSVWCYLIMALSRLSILEMFCPLFGSGADSVWCERSDFTT 180
QY 196 IAMVFLCVLCCSSLVLLVRLICGSRKMLFRLVYTLITLVFLALCGLPFGIOMALFS 255
Db 181 IAMVFLCVLCCSSLVLLVRLICGSRKMLFRLVYTLITLVFLALCGLPFGIOMALFS 240
QY 256 RIHLDKVLFCVHVLVSLFSLANSSANPIYFVGSFRORONRMLKVLQALQDPE 315
Db 241 RIHLDKVLFCVHVLVSLFSLANSSANPIYFVGSFRORONRMLKVLQALQDPE 300
QY 316 VDEGGWLPORTELHSGSRLEQ 337
Db 301 VDEGGWLPORTELHSGSRLEQ 322

RESULT 5
AD116993
ID AD116993 standard; protein; 322 AA.
XX
AC AD116993;
XX
DT 15-APR-2004 (first entry)
XX
DE Human NOXV protein homologue SeqID 529.
XX
KW human; NOXV; cardiomyopathy; atherosclerosis; cancer; diabetes;
inflammation; autoimmune disorder; allergy; blood disorder;
acquired immunodeficiency syndrome; AIDS; obesity; asfama;
immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
Alzheimer's disease; infection; scr.
XX
OS Homo sapiens.
XX
PN WO200268649-A2.
XX
PD 06-SEP-2002.
XX
PF 31-JAN-2002; 2002WO-US002785.
XX
PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 08-FEB-2001; 2001US-0267057P.
PR 09-FEB-2001; 2001US-0267459P.
PR 15-FEB-2001; 2001US-0268723P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278653P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.

PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.
XX
PA Tchernev VT, Spytek KA, Zernusen BD, Paturajan M, Shinkes RA;
PI Li L, Gangoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grose WM, Alebrock JP, Lepley DM, Rieger DK, Burgess CB;
XX
PS MPI; 2002-706998/76.
XX
XX New NOXV polypeptides and nucleic acids, useful for preventing or
PT treating NOXV-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
PS Disclosure; SEQ ID NO 529; 1498pp; English.

This invention relates to a novel nucleic acids, and encoded polypeptides
therof, which have properties related to the stimulation of biochemical
or physiological responses in a cell, tissue, organ or organism.
Specifically, it refers to the use of biologically active fragments for
diagnostic and prognostic assays and furthermore in the treatment of
diverse pathological conditions. The present invention describes novel
human and murine NOXV proteins, as well as methods to modulate their
expression using antisense oligos, ribozymes and peptide nucleic acids.
The NOXV polypeptides, polynucleotides and antibodies are useful in
treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
atherosclerosis, cancer and diabetes. Furthermore, they may be used in
treating or preventing diseases such as inflammation, autoimmune
disorders, allergies, blood disorders, acquired immunodeficiency syndrome
(AIDS), obesity, asfama, immunoglobulin (Ig)A nephropathy, cirrhosis,
arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
and epilepsy. Accordingly, these molecules have many activities including
cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
neuroprotective, neurotropic, antibacterial, virocidic, antiparasitic,
relaxant and anticonvulsant. In addition, they are useful in screening
assays to identify small molecules that modulate or inhibit, for example,
neurogenesis, wound healing and angiogenesis. The nucleic acids are also
used as in chromosome mapping, tissue typing, preventive medicine and
pharmacogenomics. This polypeptide is a homologue of a human NOXV protein
of the invention.

Query Match

95.7%; Score 1688; DB 5; Length 322;

Best Local Similarity 100.0%; Pred. No. 1.2e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 16 MDSTIPVLGELTPINREETPCQKLTFTGLTCTVSLATNGNAVVMILGCRMRNA 75
Db 1 MDSTIPVLGELTPINREETPCQKLTFTGLTCTVSLATNGNAVVMILGCRMRNA 60
QY 76 VSIYIINLVADEFLSGHIIICSPRLINIRHPISKILSPVMTFPYIGLSMLSAISTER 135
Db 61 VSIYIINLVADEFLSGHIIICSPRLINIRHPISKILSPVMTFPYIGLSMLSAISTER 120
QY 136 CLSILPMTWCHCRPRYLSSVMCVLLMALSLNSILEMFCDFLPSGADSVWCETSDFIT 195
Db 121 CLSILPMTWCHCRPRYLSSVMCVLLMALSLNSILEMFCDFLPSGADSVWCETSDFIT 180
QY 196 IANLVPLCVLCCSSLVLRILCGSRKMPRLTYTITLTVALVPLCGLPFGIQVALFS 255
Db 181 IANLVPLCVLCCSSLVLRILCGSRKMPRLTYTITLTVALVPLCGLPFGIQVALFS 240
QY 256 RIHDMKVLFCFHVLTSLFSLALSSANPITTFVSGFRORONRKLVLQRALQDTPR 315
Db 241 RIHDMKVLFCFHVLTSLFSLALSSANPITTFVSGFRORONRKLVLQRALQDTPR 300
QY 316 VDEGGGWLPOETLELSSGRLEQ 337
Db 301 VDEGGGWLPOETLELSSGRLEQ 322
```

RESULT 6
AD116998
ID AD116998 standard; protein; 322 AA.

AC AD116998;

DT 15-APR-2004 (first entry)

DE Human NOVX protein homologue Segid 534.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;

KW inflammation; autoimmune disorder; allergy; blood disorder;

KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;

KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;

KW Alzheimer's disease; infection; str.

OS Homo sapiens.

PN WO200268649-A2.

PD 06-SEP-2002.

XX 31-JAN-2002; 2002MO-US002785.

XX 31-JAN-2001; 2001US-0265395P.

XX 31-JAN-2001; 2001US-0265412P.

XX 31-JAN-2001; 2001US-0265514P.

XX 31-JAN-2001; 2001US-0265517P.

XX 02-FEB-2001; 2001US-0266406P.

XX 07-FEB-2001; 2001US-0266767P.

XX 07-FEB-2001; 2001US-0267057P.

XX 08-FEB-2001; 2001US-0267459P.

XX 09-FEB-2001; 2001US-0267823P.

XX 15-FEB-2001; 2001US-0268974P.

XX 26-FEB-2001; 2001US-0271664P.

XX 27-FEB-2001; 2001US-0271839P.

XX 02-MAR-2001; 2001US-0271855P.

XX 02-MAR-2001; 2001US-0272788P.

XX 14-MAR-2001; 2001US-0273046P.

XX 14-MAR-2001; 2001US-0273925P.

XX 14-MAR-2001; 2001US-0275947P.

XX 14-MAR-2001; 2001US-0275950P.

XX 14-MAR-2001; 2001US-0275989P.

XX 15-MAR-2001; 2001US-0276448P.

PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 26-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0290447P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 15-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.

XX Tchernev VT, Spytek KA, Zernusen BD, Patnrajan M, Shinkets RA;

XX Li L, Gangolli EA, Padgaru M, Anderson DM, Raetelli L, Miller CE;

PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CRA;

PI Pirtak K, Grosse WM, Alsbrook UF, Lepley DM, Rieger DK, Burgess CB;

XX WPI; 2002-706998/76.

XX New NOVX polypeptides and nucleic acids, useful for preventing or

PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,

PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX Disclosure; SEQ ID NO 534; 1498bp; English.

XX This invention relates to a novel nucleic acid, and encoded polypeptides

CC thereof, which have properties related to the stimulation of biochemical

CC or physiological responses in a cell, tissue, organ or organism.

CC Specifically, it refers to the use of biologically active fragments for

CC diagnostic and prognostic assays and furthermore in the treatment of

CC diverse pathological conditions. The present invention describes novel

CC human and murine NOVX proteins, as well as methods to modulate their

CC expression using antisense oligos, ribozymes and peptide nucleic acids.

CC The NOVX polypeptides, polynucleotides and antibodies are useful in

CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,

CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in

CC treating or preventing diseases such as inflammation, autoimmune

CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome

CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,

CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy

CC and epilepsy. Accordingly, these molecules have many activities including

CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,

CC hemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,

CC antisthmatic, nephrotropic, antiarthritic, hepatotropic,

CC neuroprotective, nootropic, antibacterial, viricide, antiparasitic,

CC relaxant and anticonvulsant. In addition, they are useful in screening

CC assays to identify small molecules that modulate or inhibit, for example,

CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also

CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.
XX

SO Sequence 322 AA:

Query Match 95.7%; Score 1688; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.2e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

16 MDSTIPVLTGTELTPTNGREBTPCYKOTLSFTGLTCIVSLVATGNVAVMLGCMRRNA 75
DB 1 MDSTIPVLTGTELTPTNGREBTPCYKOTLSFTGLTCIVSLVATGNVAVMLGCMRRNA 60
QY 76 VSIYILNVADPFLSGHIICSPRLINIRHPISKILSPWTFPPYIGLSMISAISTER 135
DB 61 VSIYILNVADPFLSGHIICSPRLINIRHPISKILSPWTFPPYIGLSMISAISTER 120
QY 136 CLSTLMPWYHCRPRRYLSSVWCVLMLSLRSLIEMWFCDFLFGADSWCETSDFIT 195
DB 121 CLSTLMPWYHCRPRRYLSSVWCVLMLSLRSLIEMWFCDFLFGADSWCETSDFIT 180
QY 196 IAMVFLCVVCGSSLVLVRLICGSRKMPRLRYVITLTVLVLGSLPFGIQMALFS 255
DB 181 IAMVFLCVVCGSSLVLVRLICGSRKMPRLRYVITLTVLVLGSLPFGIQMALFS 240
QY 256 RIHLDKVLFCFHVHVSIFLSALNSSANPIIYFVGFRRORONKLVLRALQDTPPE 315
DB 241 RIHLDKVLFCFHVHVSIFLSALNSSANPIIYFVGFRRORONKLVLRALQDTPPE 300
QY 316 VDEGGWLPQETLBSGRLEQ 337
DB 301 VDEGGWLPQETLBSGRLEQ 322

RESULT 7

ABP81750
ID ABP81750 standard; protein; 322 AA.

XX AC ABP81750;

XX DT 04-MAR-2003 (first entry)

DE Human G protein-coupled receptor MrgX3 protein SEQ ID NO:674.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hyperextension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer.

XX Homo sapiens.

XX PN W0200261087-A2.

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US050107.

XX PR 19-DEC-2000; 2000US-0257144P.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burnet GC, Roush CL, Brown JP;

XX DR WPI; 2003-046718/04.

XX N-PSDB; ABZ42595.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

PS Disclosure: Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. ABZ42593 to ABZ42869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention

SO Sequence 322 AA:

Query Match 95.7%; Score 1688; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.2e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVLTGTELTPTNGREBTPCYKOTLSFTGLTCIVSLVATGNVAVMLGCMRRNA 75
DB 1 MDSTIPVLTGTELTPTNGREBTPCYKOTLSFTGLTCIVSLVATGNVAVMLGCMRRNA 60
QY 76 VSIYILNVADPFLSGHIICSPRLINIRHPISKILSPWTFPPYIGLSMISAISTER 135
DB 61 VSIYILNVADPFLSGHIICSPRLINIRHPISKILSPWTFPPYIGLSMISAISTER 120
QY 136 CLSTLMPWYHCRPRRYLSSVWCVLMLSLRSLIEMWFCDFLFGADSWCETSDFIT 195
DB 121 CLSTLMPWYHCRPRRYLSSVWCVLMLSLRSLIEMWFCDFLFGADSWCETSDFIT 180
QY 196 IAMVFLCVVCGSSLVLVRLICGSRKMPRLRYVITLTVLVLGSLPFGIQMALFS 255
DB 181 IAMVFLCVVCGSSLVLVRLICGSRKMPRLRYVITLTVLVLGSLPFGIQMALFS 240
QY 256 RIHLDKVLFCFHVHVSIFLSALNSSANPIIYFVGFRRORONKLVLRALQDTPPE 315
DB 241 RIHLDKVLFCFHVHVSIFLSALNSSANPIIYFVGFRRORONKLVLRALQDTPPE 300
QY 316 VDEGGWLPQETLBSGRLEQ 337
DB 301 VDEGGWLPQETLBSGRLEQ 322

RESULT 8

ADH08535
ID ADH08535 standard; protein; 322 AA.

XX AC ADH08535;

XX DT 25-MAR-2004 (first entry)

DE MrGX3.
XX mas-related gene D; MrGD; Analgesic; Vulnerary; Ophthalmological;
KM sensory perception; glaucoma; MrG.
XX
XX Mus musculue.
XX
XX MO2004003133-A1.
XX
XX 08-JUN-2004.
XX
XX 13-MAY-2003; 2003MO-US015004.
XX
XX 26-JUN-2002; 2002US-00183116.
XX
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Anderson DJ, Dong X, Zylka M, Han S, Simon MI;
XX
XX WPI; 2004-083025/08.
XX
XX N-PSDB; ADH08534.
XX
XX New mas-related gene D polypeptides, useful as therapeutics or in
XX identifying agonists or antagonists that alter pain perception in a
XX mammal for treating impaired sensory perception, e.g. chronic intractable
XX pain or neuropathic pain.
XX
XX disclosure; SEQ ID NO 31; 220pp; English.
XX
XX The present invention relates to an isolated mas-related gene D (MrGD)
XX polypeptide. The MrGD polypeptides are useful as therapeutics or for
XX identifying compounds, i.e. agonists or antagonists, that alter pain
XX perception in a mammal. The compounds are useful for treating impaired
XX sensory perception, e.g. chronic intractable pain or neuropathic pain,
XX promoting wound healing, restoring normal sensitivity following injury,
XX or treating ocular conditions, particularly those associated with
XX pressure such as glaucoma. The MrG genes or proteins may be used as
XX molecular probes for the detection of cells or tissues related to or
XX involved with sensory perception. The present sequence represents a MrGA
XX (MrG subfamily) protein.
XX
XX Sequence 322 AA:
SQ
Query Match 95.7%; Score 1688; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.2e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MDSTIPLVLTGTELPINGREETPCYKOTLSTFTGLTCTIVSLVATGNNAVLMLGCRMRNA 75
DB 1 MDSTIPLVLTGTELPINGREETPCYKOTLSTFTGLTCTIVSLVATGNNAVLMLGCRMRNA 60
QY 76 VSIYIINLVAADEPLFSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 135
DB 61 VSIYIINLVAADEPLFSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 120
QY 136 CTSILPPIWYHCRPRYLSSVMCVLMALSLASIIEMWPCDPLFGADSVWCETSDFIT 195
DB 121 CTSILPPIWYHCRPRYLSSVMCVLMALSLASIIEMWPCDPLFGADSVWCETSDFIT 180
QY 196 IAMLVFLCVVLCSSSLVTLVRIICGSRKMPLTRLYTILITVAVFLCGLPFGIOWALFS 255
DB 181 IAMLVFLCVVLCSSSLVTLVRIICGSRKMPLTRLYTILITVAVFLCGLPFGIOWALFS 240
QY 256 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFVGSFRORONRKIKVLOALODTPE 315
DB 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFVGSFRORONRKIKVLOALODTPE 300
QY 316 VDEGGMLPOETLELSSRLQ 337
DB 301 VDEGGMLPOETLELSSRLQ 322
RESULT 9

AD044602
ID ADO44602 standard; protein; 322 AA.
XX
XX ADO44602;
AC
XX 29-JUL-2004 (first entry)
DT
XX
XX Human HIT7213 protein.
DE
XX
XX HIT7213; transgenic; G protein-coupled receptor; GPCR; ophthalmological;
KM cytoabatic; nephrotoxic; antiinflammatory; dermatological; analgesic;
KM vulnerary; neuroprotective; human; receptor.
XX
XX Homo sapiens.
XX
XX MO2004039972-A1.
XX
XX 13-MAY-2004.
XX
XX 28-OCT-2003; 2003MO-JP013781.
XX
XX 29-OCT-2002; 2002JP-00314141.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Kaisho Y, Watanabe T, Yasuhara Y, Mori I, Takeomi S;
XX
XX WPI; 2004-376191/35.
XX
XX N-PSDB; ADO44603.
XX
XX HIT7213 protein, encoded DNA and transgenic animals for clarifying
XX pathological mechanism, developing therapeutic methods and screening
XX preventives or remedies for related diseases e.g. cataract, cancer, and
XX dermatitis.
XX
XX Claim 3; SEQ ID NO 1; 161pp; Japanese.
XX
XX The invention relates to a non-human mammal that carries a DNA integrated
XX with a foreign HIT7213 or its mutant gene, or a part of it. The non-human
XX animal is particularly a rat. Such gene shows phenotypes of e.g. cataract
XX onset, transient skin rash and proliferation-promoting activity. The
XX foreign HIT7213 gene is a gene that encodes a G protein-coupled receptor
XX (GPCR) protein HIT7213. The protein, its encoded DNA and constructed
XX transgenic animals are useful for clarifying pathological mechanism,
XX developing therapeutic methods and screening preventives or remedies for
XX related diseases e.g. cataract, cancer, and dermatitis. The present
XX sequence represents a human HIT7213 protein.
XX
XX Sequence 322 AA:
SQ
Query Match 95.7%; Score 1688; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.2e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MDSTIPLVLTGTELPINGREETPCYKOTLSTFTGLTCTIVSLVATGNNAVLMLGCRMRNA 75
DB 1 MDSTIPLVLTGTELPINGREETPCYKOTLSTFTGLTCTIVSLVATGNNAVLMLGCRMRNA 60
QY 76 VSIYIINLVAADEPLFSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 135
DB 61 VSIYIINLVAADEPLFSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 120
QY 136 CTSILPPIWYHCRPRYLSSVMCVLMALSLASIIEMWPCDPLFGADSVWCETSDFIT 195
DB 121 CTSILPPIWYHCRPRYLSSVMCVLMALSLASIIEMWPCDPLFGADSVWCETSDFIT 180
QY 196 IAMLVFLCVVLCSSSLVTLVRIICGSRKMPLTRLYTILITVAVFLCGLPFGIOWALFS 255
DB 181 IAMLVFLCVVLCSSSLVTLVRIICGSRKMPLTRLYTILITVAVFLCGLPFGIOWALFS 240
QY 256 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFVGSFRORONRKIKVLOALODTPE 315
DB 241 RIHLDWKVLFCHVHLVSIPLSALNSSANPIIYFVGSFRORONRKIKVLOALODTPE 300

QY 316 VDEGGWLPQETLEISGRLEQ 337
 DB 301 VDEGGWLPQETLEISGRLEQ 322
 RESULT 10
 ADO29705
 ID ADO29705 standard; protein; 322 AA.
 AC ADO29705;
 XX
 DT 29-JUL-2004 (first entry)
 DE Human GPCR MEGX3, SEQ ID NO:807.
 XX
 G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KM transgenic mouse; neurological disorder; adrenal gland disorder;
 KM colon disorder; intestinal disorder; cardiovascular disorder;
 KM muscular disorder; blood disorder; immune disorder; bone disorder;
 KM joint disorder; metabolic disorder; nutritive disorder; cancer;
 KM kidney disorder; liver disorder; lung disorder; breast disorder;
 KM ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KM skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KM thymus disorder; thyroid disorder; antiparkinsonian; antitumor;
 KM cytoskeletal; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KM CNS; central nervous system; respiratory; antidiarrhetic; antidiabetic;
 KM virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KM dermatological; antitumor; antihypertensive; anorectic;
 KM immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
 KM receptor.
 OS Homo sapiens.
 XX
 PN MO2004040000-A2.
 PD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003WO-US028226.
 XX
 PR 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 PA (PRIM-) PRIMAL INC.
 PI Galtanaris GA, Bergmann JB, Gragerov A, Hohmann J, Li F,
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX
 DR WPI; 2004-339329/36.
 DR N-PSDB; ADO30080.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 PS Claim 151; SEQ ID NO 807; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,

CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 322 AA;
 QY
 Db 16 MDSTIPVAGTELTTPINGREETPCYKQTLSPFGLCTIVSLVATGNAVVLMLGCRMRNA 75
 1 MDSTIPVAGTELTTPINGREETPCYKQTLSPFGLCTIVSLVATGNAVVLMLGCRMRNA 60
 QY 76 VSIYILNVAADPLFLSGHIIICSPRLINIRHPIISKILSPVMTPEYFGISMLSAISTER 135
 61 VSIYILNVAADPLFLSGHIIICSPRLINIRHPIISKILSPVMTPEYFGISMLSAISTER 120
 Db 136 CLSITIPWYHGRPRRYSWCVLWNLISRLSILEMFCDFLFGSADSVWCETSPFIT 195
 121 CLSITIPWYHGRPRRYSWCVLWNLISRLSILEMFCDFLFGSADSVWCETSPFIT 180
 QY 196 IAMLVFLCVLGGSLVLYVILGSRKMPETRLTYVITLTVLFLICGLPFGIOMALFS 255
 181 IAMLVFLCVLGGSLVLYVILGSRKMPETRLTYVITLTVLFLICGLPFGIOMALFS 240
 QY 256 RIHLDMKVLFGVHLVSIPLSALNSANPIIYFVGSFRRORONRQNLKVLQRALQDTPPE 315
 241 RIHLDMKVLFGVHLVSIPLSALNSANPIIYFVGSFRRORONRQNLKVLQRALQDTPPE 300
 Db 316 VDEGGWLPQETLEISGRLEQ 337
 301 VDEGGWLPQETLEISGRLEQ 322
 QY
 Db 301 VDEGGWLPQETLEISGRLEQ 322
 RESULT 11
 ADF70481
 ID ADF70481 standard; protein; 560 AA.
 AC ADF70481;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 XX Orphan receptor ligand-related human protein Segid104.
 XX
 XX ligand; orphan receptor protein; fusion protein; fluorescent protein;
 KM cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
 KM GFPuv; Enhanced GFP; EGFP; human.
 OS Homo sapiens.
 XX
 PN WO2003071272-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 21-FEB-2003; 2003WO-JP001901.
 XX
 PR 22-FEB-2002; 2002JP-00045728.
 PR 23-JUL-2002; 2002JP-00213949.
 PR 11-OCT-2002; 2002JP-00298237.

XX (TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX WPI; 2003-697654/66.
XX DR N-PSDB; ADF70583.
XX
XX Transformation of cells with a fusion protein of an orphan receptor
XX PT protein with a fluorescent protein useful for identification of ligands
XX PT to the orphan receptor.
XX
XX Disclosure; SEQ ID NO 104; 594pp; Japanese.
XX
XX This invention relates to a novel method of identifying ligands to an
XX CC orphan receptor protein which comprises transforming cells with DNA
XX CC encoding a fusion protein of the orphan receptor with a fluorescent
XX CC protein, so that the fusion protein is expressed in the cells (or cell
XX CC membranes isolated from them) and contacting the cells with the potential
XX CC ligand to be tested. A suitable fluorescent protein for incorporation in
XX CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
XX CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
XX CC identification of ligands binding to an orphan receptor protein.
XX
SQ Sequence 560 AA;
Query Match 95.7%; Score 1688; DB 7; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.4e-172;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MDSTIPVLGTELPIPINGRETPCYKOTLSFTGLTCTIVSLVATGNNAVLMLCGRMRNA 75
DB 1 MDSTIVLGTGLTPIPINGRETPCYKOTLSFTGLTCTIVSLVATGNNAVLMLCGRMRNA 60
QY 76 VSIYIINLVADPLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
DB 61 VSIYIINLVADPLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 120
QY 136 CSTILMPWYHCRPRYLSSVMCVLMLSLRSIIEMFCDPLFGADSVWCETSPFIT 195
DB 121 CSTILMPWYHCRPRYLSSVMCVLMLSLRSIIEMFCDPLFGADSVWCETSPFIT 180
QY 196 IAMLVFLCVLTCSSSLVLRILICGSRKMPRLTYTILTVLVFLCGLPFGIOMALFS 255
DB 181 IAMLVFLCVLTCSSSLVLRILICGSRKMPRLTYTILTVLVFLCGLPFGIOMALFS 240
QY 256 RIHLDMKVLFCCHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALQDTPPE 315
DB 241 RIHLDMKVLFCCHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALQDTPPE 300
QY 316 VDEGGGMLPOETIELSGSRLEQ 337
DB 301 VDEGGGMLPOETIELSGSRLEQ 322
RESULT 12
AA90762
ID AAY90762 standard; protein; 322 AA.
XX
XX AAY90762;
XX
XX 18-AUG-2000 (first entry)
XX DT
XX Human G protein-coupled receptor hMT7213V SEQ ID NO:2.
XX DE
XX Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
XX KM genetic disease; cellular function regulation.
XX KM
XX Homo sapiens.
XX OS
XX PN MO200020455-A1.
XX PD 13-APR-2000.

XX 30-SEP-1999; 99MO-JP005366.
XX
XX 01-OCT-1998; 98JP-00279535.
XX
XX (TAKEDA CHEM IND LTD.
XX PA
XX Matanabe T, Terao Y, Matsui H;
XX PI WPI; 2000-303747/26.
XX DR N-PSDB; AAA29812.
XX
XX Human-derived G protein-coupled protein and encoding nucleic acid, useful
XX PT e.g. in determining ligands and treatment of diseases associated with
XX PT dysfunction of the protein.
XX
XX Claim 2; Page 92-93; 97pp; Japanese.
XX
XX The present sequence represents a human-derived G protein-coupled protein
XX CC designated hMT7213V, which is isolated from the human hippocampus. The G
XX CC protein-coupled receptor can be used for preventing, treating and
XX CC diagnosing genetic diseases associated with G protein-coupled protein,
XX CC and for regulating cellular functions. The protein can be used to prevent
XX CC and treat disorders associated with G protein-coupled protein gene
XX CC dysfunction. It can also be used to identify G protein-coupled protein
XX CC ligands and generating antibodies and antisera against the protein. It is
XX CC also useful in constructing recombinant receptor protein expression
XX CC systems, developing receptor-binding assay systems and screening drug
XX CC candidates, and can be used as a probe in the genetic diagnosis of G
XX CC protein-coupled protein disorders
XX
SQ Sequence 322 AA;
Query Match 95.5%; Score 1683; DB 3; Length 322;
Best Local Similarity 99.7%; Pred. No. 4.1e-172;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 16 MDSTIPVLGTELPIPINGRETPCYKOTLSFTGLTCTIVSLVATGNNAVLMLCGRMRNA 75
DB 1 MDSTIVLGTGLTPIPINGRETPCYKOTLSFTGLTCTIVSLVATGNNAVLMLCGRMRNA 60
QY 76 VSIYIINLVADPLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
DB 61 VSIYIINLVADPLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 120
QY 136 CSTILMPWYHCRPRYLSSVMCVLMLSLRSIIEMFCDPLFGADSVWCETSPFIT 195
DB 121 CSTILMPWYHCRPRYLSSVMCVLMLSLRSIIEMFCDPLFGADSVWCETSPFIT 180
QY 196 IAMLVFLCVLTCSSSLVLRILICGSRKMPRLTYTILTVLVFLCGLPFGIOMALFS 255
DB 181 IAMLVFLCVLTCSSSLVLRILICGSRKMPRLTYTILTVLVFLCGLPFGIOMALFS 240
QY 256 RIHLDMKVLFCCHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALQDTPPE 315
DB 241 RIHLDMKVLFCCHVLVSIPLSALNSSANPIIYFVGSFRORONRQMLKVLQALQDTPPE 300
QY 316 VDEGGGMLPOETIELSGSRLEQ 337
DB 301 VDEGGGMLPOETIELSGSRLEQ 322
RESULT 13
AD116994
ID AD116994 standard; protein; 322 AA.
XX
XX AD116994;
XX AC
XX 15-APR-2004 (first entry)
XX DT
XX Human NOVX protein homologue SegID 530.
XX DE
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX KM

KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.
OS Homo sapiens.
XX WO200268649-A2.
PN 06-SEP-2002.
XX 31-JAN-2002; 2002WO-US002785.
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 08-FEB-2001; 2001US-0267057P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 29-MAR-2001; 2001US-0280147P.
XX 30-MAR-2001; 2001US-0280192P.
XX 11-APR-2001; 2001US-0282992P.
XX 11-APR-2001; 2001US-0283083P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296944P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312028P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312908P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.
XX 31-AUG-2001; 2001US-0316447P.
XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318118P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323379P.
XX 18-OCT-2001; 2001US-0330245P.
XX 18-OCT-2001; 2001US-0330308P.
XX 14-NOV-2001; 2001US-0332701P.
XX (CURA-) CURAGEN CORP.
XX Tehernev VT, Sopytek KA, Zernusen BD, Patnurajan M, Shinketa RA;
PI Li L, Gangolli EA, Padigaru M, Rastelli L, Miller CE;
PI Gerlach VL, Taupier Ku, Gusev VT, Colman SD, Molenc AK, Pena CBA;

PI Putrak K, Groose WM, Alsebrook JP, Lepley DM, Rieger DK, Burgess CE;
XX WPI; 2002-706998/76.
XX New NOXV polypeptides and nucleic acids, useful for preventing or
PT treating NOXV-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX Disclosure; SEQ ID NO 530; 1498bp; English.
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOXV proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOXV polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
CC antiasthmatic, nephrotoxic, antihypertensive, hepatocytotoxic,
CC neuroprotective, neurotropic, antibacterial, vitruce, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOXV protein
CC of the invention.
XX
XX Sequence 322 AA;
SQ
Query Match 95.5%; Score 1683; DB 5; Length 322;
Beat Local Similarity 99.7%; Pred. No. 4,1e-172;
Matches 321; Conservative 1; Mismatches 0; Gaps 0;
Indels 0;
QY 16 MDSITPVLTGTELTPIINGREETPCYKQTLSTFTGTCIVSLVATGNVAVLMLGCRMRNA 75
DB 1 MDSITPVLTGTELTPIINGREETPCYKQTLSTFTGTCIVSLVATGNVAVLMLGCRMRNA 60
QY 76 VSIYILNIVAADPFLSGHITCSPLRLINRHPISKILSPMPMPPTGISMASSTER 135
DB 61 VSIYILNIVAADPFLSGHITCSPLRLINRHPISKILSPMPMPPTGISMASSTER 120
QY 136 CTSILMPITWYHCRPRRYLSSVMCVLWALSLRSLILSMFCDPLFGSGADSVWCSTSDPIT 195
DB 121 CTSILMPITWYHCRPRRYLSSVMCVLWALSLRSLILSMFCDPLFGSGADSVWCSTSDPIT 180
QY 196 IAWLFLCVLTCGSSSLVLVRLILGSRMPYTRLYVTLLTVLVELLGLSPFGIOWALFS 255
DB 181 IAWLFLCVLTCGSSSLVLVRLILGSRMPYTRLYVTLLTVLVELLGLSPFGIOWALFS 240
QY 256 RIHLDWKTLFCHVHLVSTFSLNLSANPITTFVGSFRORORONKYLQALDPTPE 315
DB 241 RIHLDWKTLFCHVHLVSTFSLNLSANPITTFVGSFRORORONKYLQALDPTPE 300
QY 316 VDEGGWLPQETLELSSRLAQ 337
DB 301 VDEGGWLPQETLELSSRLAQ 322
RESULT 14
AD116999
ID AD116999 standard; protein; 322 AA.
XX

AC AD16999;
XX
DT 15-APR-2004 (first entry)
XX
XX Human NOVX protein homologue Segid 535.
DE
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; str.
XX Homo sapiens.
XX
XX MO200268649-A2.
XX
PD 06-SEP-2002.
XX
PF 31-JAN-2002; 2002MO-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0276652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278778P.
XX 29-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282992P.
XX 11-APR-2001; 2001US-0283083P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296964P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312908P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.
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XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318118P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323379P.
XX 18-OCT-2001; 2001US-0330245P.
XX 18-OCT-2001; 2001US-0330308P.

PR 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernev VT, Spytek KA, Zernhusen BD, Paturajan M, Shinkens RA;
PI La L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CB;
PI Gerlach VL, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grosse WM, Alsbrook JF, Lepley DM, Rieger DK, Burgess CE;
XX
XX WPI; 2002-706998/76.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Disclosure, SEQ ID NO 535; 1498bp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, anti-inflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
CC antiaesthetic, nephroprotective, anticholesteric, hepatotropic,
CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.
XX
XX Sequence 322 AA;
SQ
Query Match 95.5%; Score 1683; DB 5; Length 322;
Best Local Similarity 99.7%; Pred. No. 4,1e-172;
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 16 MSTIYVLTGTELPINGRETPCYKOTLSPTGTCTVSLVATLGNVVMMLGCRMRNA 75
DB 1 MSTIYVLTGTELPINGRETPCYKOTLSPTGTCTVSLVATLGNVVMMLGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHICSPRLINIRHPSKILSPVMTFPFIFGISMALSTER 135
DB 61 VSIYIINLVAAADFLPSGHICSPRLINIRHPSKILSPVMTFPFIFGISMALSTER 120
QY 136 CLSILWPIWYHCRPRYLSVVCVLMALSLRSILEMFCDFLFGSGADSVWCETSDFIT 195
DB 121 CLSILWPIWYHCRPRYLSVVCVLMALSLRSILEMFCDFLFGSGADSVWCETSDFIT 180
QY 196 IAWLVFLCVVLCSSVLVLRILCSGRKMPRLRYTITLLTVLVFLCGIPRIGIOWALFS 255
DB 181 IAWLVFLCVVLCSSVLVLRILCSGRKMPRLRYTITLLTVLVFLCGIPRIGIOWALFS 240
QY 256 RIHLDMKVLFCFVHLVSIIFLSALNSSANPIYFVGSFROKORNLKVLQBALDPTFS 315
DB 241 RIHLDMKVLFCFVHLVSIIFLSALNSSANPIYFVGSFROKORNLKVLQBALDPTFS 300
QY 316 VDEGGMLPQETLLESGRLAQ 337
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Db 301 VDEGGWLPQETLBSGSRLQ 322

RESULT 15

ID ADC86821 standard; protein; 322 AA.

AC ADC86821;

DT 01-JAN-2004 (first entry)

DE Human GPCR protein SEQ ID NO:1274.

human; GPCR; guanosine triphosphate-binding protein coupled receptor; gene therapy.

OS Homo sapiens.

PN EPI270724-A2.

PD 02-JAN-2003.

PF 18-JUN-2002; 2002EP-00013517.

PR 18-JUN-2001; 2001JP-00246789.

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

PI Suwa M, Asai K, Akiyama Y, Aburatani H;

DR WPI; 2003-315783/31.

DR N-PSDB; ADC86820.

PT New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.

PS Claim 2; SEQ ID NO 1274; 28bp; English.

CC The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.

XX Sequence 322 AA;

Query Match 95.5%; Score 1683; DB 7; Length 322;

Best Local Similarity 99.7%; Pred. No. 4.1e-172;

Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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1 MDSTIPVLGTELPTINGREETPCYKOTLSFTGLTCTIVSLVATGNAVVMILGCMRRNA 60

76 VSIYILNVADPLFLSGHIIICSPRLINIRHPISKIISPVMTPEYPTGLSMISAISTER 135

61 VSIYILNVADPLFLSGHIIICSPRLINIRHPISKIISPVMTPEYPTGLSMISAISTER 120

136 CLSTLMPITWYHCRPRYSVYVCLLMLSLSLILEMWFCDPLFSGADSVWCETSDFTT 195

121 CLSTLMPITWYHCRPRYSVYVCLLMLSLSLILEMWFCDPLFSGADSVWCETSDFTT 180

196 IAWLVFLCVLGGSSLVLLVRLICGSRKMPLTRLYVTILLTVLVFLCGLPFGIQWALFS 255

181 IAWLVFLCVLGGSSLVLLVRLICGSRKMPLTRLYVTILLTVLVFLCGLPFGIQWALFS 240

256 RIHIDWKVLFCHVHLVSIFLSALNSSANPIITYFVGSRFRORONRNLKLVLRALQDTPR 315

241 RIHIDWKVLFCHVHLVSIFLSALNSSANPIITYFVGSRFRORONRNLKLVLRALQDTPR 300

Qy 316 VDEGGWLPQETLBSGSRLQ 337

Db 301 VDEGGWLPQETLBSGSRLQ 322

Search completed: October 27, 2004, 08:30:17
Job time : 160 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2004, 08:24:28 : Search time 40 Seconds
(without alignments)
558.729 Million cell updates/sec

Title: US-09-867-570-2

Perfect score: 1763

Sequence: 1 MSKSSWVIRLGLSMDSTI.....EGGWLPGETLISGSRLEQ 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- 1: Issued Patents AA:*
- 2: /cgn2_6/prodata/1/aa/5A COMB.pep:*
- 3: /cgn2_6/prodata/1/aa/5B COMB.pep:*
- 4: /cgn2_6/prodata/1/aa/6A COMB.pep:*
- 5: /cgn2_6/prodata/1/aa/6B COMB.pep:*
- 6: /cgn2_6/prodata/1/aa/PCTUS COMB.pep:*
- 7: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1642	93.1	322	4	US-09-254-227A-3 Sequence 3, Appl1
2	1598	90.6	322	4	US-09-254-227A-5 Sequence 5, Appl1
3	1405	79.7	322	4	US-09-254-227A-7 Sequence 7, Appl1
4	1391	78.9	322	4	US-09-254-227A-9 Sequence 9, Appl1
5	1379	78.2	322	4	US-09-254-227A-11 Sequence 11, Appl1
6	1360	77.1	322	4	US-09-254-227A-13 Sequence 13, Appl1
7	834.5	47.3	337	4	US-09-254-227A-1 Patent No. 5320941
8	423.5	24.0	325	6	US-08-118-270-52 Sequence 52, Appl1
9	388.5	22.0	282	5	PCT-US93-08528-52 Sequence 52, Appl1
10	388.5	22.0	282	5	PCT-US93-08528-52 Sequence 76, Appl1
11	344	19.5	298	1	US-08-118-270-76 Sequence 76, Appl1
12	344	19.5	298	5	PCT-US93-08528-76 Sequence 76, Appl1
13	255.5	14.5	335	3	US-08-981-825-6 Sequence 6, Appl1
14	255.5	14.5	335	3	US-09-480-784-6 Sequence 6, Appl1
15	235.5	13.4	354	1	US-07-759-568-2 Sequence 2, Appl1
16	230.5	13.1	381	4	US-09-745-842-21 Sequence 21, Appl1
17	226.5	12.8	335	1	US-07-759-568-1 Sequence 1, Appl1
18	226.5	12.8	335	1	US-08-450-393A-8 Sequence 8, Appl1
19	226.5	12.8	335	2	US-08-390-000A-5 Sequence 5, Appl1
20	226.5	12.8	335	3	US-08-446-669-8 Sequence 8, Appl1
21	226.5	12.8	335	4	US-09-625-573-8 Sequence 8, Appl1
22	226.5	12.8	335	5	PCT-US95-00476-8 Sequence 8, Appl1
23	226.5	12.8	335	1	US-08-202-056-7 Sequence 7, Appl1
24	226.5	12.8	360	4	US-09-409-778-4 Sequence 4, Appl1
25	219.5	12.5	369	1	US-07-816-283-8 Sequence 8, Appl1
26	219.5	12.5	369	1	US-08-417-103-8 Sequence 8, Appl1
27	219.5	12.5	369	2	US-08-411-859-3 Sequence 3, Appl1

28	219.5	12.5	369	3	US-08-120-601B-9 Sequence 9, Appl1
29	219.5	12.5	369	4	US-08-387-707-9 Sequence 9, Appl1
30	219.5	12.5	369	4	US-08-405-271A-9 Sequence 9, Appl1
31	218.5	12.4	381	1	US-08-467-125-2 Sequence 2, Appl1
32	218.5	12.4	381	2	US-08-911-320A-2 Sequence 2, Appl1
33	218.5	12.4	381	2	US-09-217-101-2 Sequence 2, Appl1
34	217	12.3	351	4	US-09-944-807-2 Sequence 2, Appl1
35	211	12.0	353	4	US-09-576-160B-6 Sequence 6, Appl1
36	210	11.9	259	4	US-09-576-159B-3 Sequence 3, Appl1
37	210	11.9	259	4	US-09-456-455A-3 Sequence 3, Appl1
38	210	11.9	380	3	US-08-676-351-5 Sequence 5, Appl1
39	206.5	11.7	384	3	US-09-071-434-3 Sequence 5, Appl1
40	206	11.7	380	3	US-08-188-275A-5 Sequence 5, Appl1
41	206	11.7	380	3	US-09-351-198-5 Sequence 5, Appl1
42	206	11.7	380	3	US-09-113-426-5 Sequence 5, Appl1
43	205.5	11.7	355	4	US-09-170-496B-2 Sequence 2, Appl1
44	205	11.6	333	4	US-09-170-496B-8 Sequence 8, Appl1
45	204	11.6	333	4	US-09-170-496B-168 Sequence 168, App

ALIGNMENTS

RESULT 1	US-09-254-227A-3	US-09-254-227A-3
Sequence 3, Appl1	Application US/09254227A	
Patent No. 6696257		
GENERAL INFORMATION:		
APPLICANT: Amad, Sultan		
APPLICANT: Banville, Denis		
APPLICANT: Fortin, Yves		
APPLICANT: Lembo, Paola		
APPLICANT: O'Donnell, Dajan		
APPLICANT: Shi-Hsiang, Shen		
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human		
FILE REFERENCE: 81823/268117		
CURRENT APPLICATION NUMBER: US/09/254,227A		
CURRENT FILING DATE: 1999-03-03		
NUMBER OF SEQ ID NOS: 22		
SOFTWARE: Patent version 3.0		
SEQ ID NO: 3		
LENGTH: 322		
TYPE: PRT		
ORGANISM: Homo sapiens		
US-09-254-227A-3		
Query Match	93.1%	Score 1642; DB 4; Length 322;
Best Local Similarity	97.2%;	Pred. No. 8.7e-138;
Matches 313; Conservative	5; Mismatches	4; Indels 0; Gaps 0;
QY	16	MDSTIVLGTETLPINGRETPCYKOTLSFTGTCIVSLVATLGNVMTLGCRRNA 75
DB	1	MDSTIVLGTETLPINGRETPCYKOTLSFTGTCIVSLVATLGNVMTLGCRRNA 60
QY	76	VSIIYINLVADPLFLSGHICSPRLINIRHPIKSLSPVMTFPYFIGLSMIASTER 135
DB	61	VSIIYINLVADPLFLSGHICSPRLINIRHPIKSLSPVMTFPYFIGLSMIASTER 120
QY	136	CSIIIMPVHCRPRYSIVMVCVLLMALSLRSIEMFCDPLFGAGDSVWCETSDFIT 195
DB	121	CSIIIMPVHCRPRYSIVMVCVLLMALSLRSIEMFCDPLFGAGDSVWCETSDFIT 180
QY	196	IAMVLVLCVYLCCSSIVLVIRIICGRKMPRLTYTTLITLVVFLCGIPRIGQALFS 255
DB	181	IAMVLVLCVYLCCSSIVLVIRIICGRKMPRLTYTTLITLVVFLCGIPRIGQALFS 240
QY	256	RHLDMKVLFCVHVLVSIFLSALNSSANPIYFVGSFROKOROMKIVLQALDTPB 315
DB	241	RHLDMKVLFCVHVLVSIFLSALNSSANPIYFVGSFROKOROMKIVLQALDTPB 300
QY	316	VDEGGWLPQETLISGSRLEQ 337
DB	301	VDEGGWLPQETLISGSRLEQ 322

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RESULT 2
US-09-254-227A-5
; Sequence 5, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-5

Query Match          90.6%; Score 1598; DB 4; Length 322;
Best Local Similarity 95.6%; Pred. No. 6.9e-134;
Matches 307; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELTPIINGREETPCYKQTLSTFTGLCTIYSLVATLGNNAVLMILGCMRRNA 75
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QY 76 VSIYIILNVADFLFLSGHIIICSPRLINIRHPISKILSPVWTFPPYFIGLSMLSAISTER 135
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QY 136 CLSILMPIMWCHRRPRLYSSVMCVLWALSLRSILEMFCDFLFGSADSVWCETSDPIT 195
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DB 121 CLSILMPIMWCHRRPRLYSSVMCVLWALSLRSILEMFCDFLFGSADSVWCETSDPIT 180

QY 196 IAWLVFLCVLGGSSVLVLRILGSRKMPRLRYVTIILTVLVFLCGLPFGIOWALFS 255
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 IAWLVFLCVLGGSSVLVLRILGSRKMPRLRYVTIILTVLVFLCGLPFGIOWALFS 240

QY 256 RIHDMKVLFCFCHVLSIFLSALNSSANPIIYFFVGSFRORONRMLKVLQALQDTPR 315
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RESULT 3
US-09-254-227A-7
; Sequence 7, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 322
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-7

Query Match          79.7%; Score 1405; DB 4; Length 322;
Best Local Similarity 83.9%; Pred. No. 8.7e-117;
Matches 270; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

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DB 1 MDPTVPVLGTELTPIINGREETPCYKQTLSTFTGLCTIYSLVATLGNNAVLMILGCMRRNA 60

QY 76 VSIYIILNVADFLFLSGHIIICSPRLINIRHPISKILSPVWTFPPYFIGLSMLSAISTER 135
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QY 136 CLSILMPIMWCHRRPRLYSSVMCVLWALSLRSILEMFCDFLFGSADSVWCETSDPIT 195
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DB 121 CLSILMPIMWCHRRPRLYSSVMCVLWALSLRSILEMFCDFLFGSADSVWCETSDPIT 180

QY 196 IAWLVFLCVLGGSSVLVLRILGSRKMPRLRYVTIILTVLVFLCGLPFGIOWALFS 255
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DB 181 IAWLVFLCVLGGSSVLVLRILGSRKMPRLRYVTIILTVLVFLCGLPFGIOWALFS 240

QY 256 RIHDMKVLFCFCHVLSIFLSALNSSANPIIYFFVGSFRORONRMLKVLQALQDTPR 315
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DB 241 WIHDMKVLFCFCHVLSIFLSALNSSANPIIYFFVGSFRORONRMLKVLQALQDTPR 300

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RESULT 4
US-09-254-227A-9
; Sequence 9, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-9

Query Match          78.9%; Score 1391; DB 4; Length 322;
Best Local Similarity 83.9%; Pred. No. 1.5e-115;
Matches 270; Conservative 16; Mismatches 36; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELTPIINGREETPCYKQTLSTFTGLCTIYSLVATLGNNAVLMILGCMRRNA 75
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDPTVPVLGTELTPIINGREETPCYKQTLSTFTGLCTIYSLVATLGNNAVLMILGCMRRNA 60

QY 76 VSIYIILNVADFLFLSGHIIICSPRLINIRHPISKILSPVWTFPPYFIGLSMLSAISTER 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 FSIYIILNVADFLFLSGRLIYSLSPISIPHTISKILYPMVMFSYFAGINFLSAVSTDR 120

QY 136 CLSILMPIMWCHRRPRLYSSVMCVLWALSLRSILEMFCDFLFGSADSVWCETSDPIT 195
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 CLSILMPIMWCHRRPRLYSSVMCVLWALSLRSILEMFCDFLFGSADSVWCETSDPIT 180

QY 196 IAWLVFLCVLGGSSVLVLRILGSRKMPRLRYVTIILTVLVFLCGLPFGIOWALFS 255
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 181 VAMLIPLFCVVLGSSSVLVLIRILICGSRKIPLTRLYTILITLVAVFLICGLPFGIQLFPL 240
Qy 256 RHLDMKVLFCFVHLVSIPLSALNSSANPIYFPFGSFRORORONLKVLOALODTPE 315
Db 241 WHHDEVEVFCFVHLVSIPLSALNSSANPIYFPFGSFRORORONLKVLOALODDAB 300
Qy 316 VDEGGGMLPOETTELSSGRL 337
Db 301 VDEGGGMLPOETTELSSGRL 322

RESULT 5
US-09-254-227A-11

Sequence 11, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-227A-11

Query Match 78.2%; Score 1379; DB 4; Length 322;
Best Local Similarity 83.4%; Pred. No. 1.8e-114;
Matches 267; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

Qy 16 MDSTIPLVGLTELPINGRETPCYKOTLSFTGLTCIVSLVLTGNAVVTMLGCRMRNA 75
Db 1 MDPTVPVFCFKLTPINGRETPCYKOTLSFTGLTCIVSLVLTGNAVVTMLGCRMRNA 60
Qy 76 VSIYIINLVADPLFISGHILICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
Db 61 VSIYIINLVADPLFISGHILICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Qy 136 CUSILMPWYHCRPRYLSSVWCVLIMALSLRSILSLEMFCDFLFGADSVWCETSDFT 195
Db 121 CUSILMPWYHCRPRYLSSVWCVLIMALSLRSILSLEMFCDFLFGADSVWCETSDFT 180
Qy 196 IAWLVFLCVVLGSSSVLVLIRILICGSRKMPLTRLYTILITLVAVFLICGLPFGIQLFPL 255
Db 181 VAMLIPLFCVVLGSSSVLVLIRILICGSRKMPLTRLYTILITLVAVFLICGLPFGIQLFPL 240
Qy 256 RHLDMKVLFCFVHLVSIPLSALNSSANPIYFPFGSFRORORONLKVLOALODTPE 315
Db 241 WHHDEVEVFCFVHLVSIPLSALNSSANPIYFPFGSFRORORONLKVLOALODDAB 300
Qy 316 VDEGGGMLPOETTELSSGRL 335
Db 301 VDEGGGMLPOETTELSSGRL 320

RESULT 6
US-09-254-227A-13

Sequence 13, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola

APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-227A-13

Query Match 77.1%; Score 1360; DB 4; Length 322;
Best Local Similarity 82.5%; Pred. No. 8.5e-113;
Matches 264; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

Qy 16 MDSTIPLVGLTELPINGRETPCYKOTLSFTGLTCIVSLVLTGNAVVTMLGCRMRNA 75
Db 1 MDPTVPVFCFKLTPINGRETPCYKOTLSFTGLTCIVSLVLTGNAVVTMLGCRMRNA 60
Qy 76 VSIYIINLVADPLFISGHILICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
Db 61 VSIYIINLVADPLFISGHILICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Qy 136 CUSILMPWYHCRPRYLSSVWCVLIMALSLRSILSLEMFCDFLFGADSVWCETSDFT 195
Db 121 CUSILMPWYHCRPRYLSSVWCVLIMALSLRSILSLEMFCDFLFGADSVWCETSDFT 180
Qy 196 IAWLVFLCVVLGSSSVLVLIRILICGSRKMPLTRLYTILITLVAVFLICGLPFGIQLFPL 255
Db 181 VAMLIPLFCVVLGSSSVLVLIRILICGSRKMPLTRLYTILITLVAVFLICGLPFGIQLFPL 240
Qy 256 RHLDMKVLFCFVHLVSIPLSALNSSANPIYFPFGSFRORORONLKVLOALODTPE 315
Db 241 WHHDEVEVFCFVHLVSIPLSALNSSANPIYFPFGSFRORORONLKVLOALODDAB 300
Qy 316 VDEGGGMLPOETTELSSGRL 335
Db 301 VDEGGGMLPOETTELSSGRL 320

RESULT 7
US-09-254-227A-1

Sequence 1, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 337
TYPE: PRT
ORGANISM: rat
US-09-254-227A-1

Query Match 47.3%; Score 834.5; DB 4; Length 337;
Best Local Similarity 52.9%; Pred. No. 3.3e-66;
Matches 174; Conservative 52; Mismatches 92; Indels 11; Gaps 6;

Qy 13 FLMSDSTIPLVGLTELPINGRETPCYKOTLSFTGLTCIVSLVLTGNAVVTMLGCRMR 72
Db 12 FVSMDEPTISLSTESTLTKTGHPC-RPILTLISFLVPIITLILGLAGNTIVMLLGFRR 70

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-52

Query Match 22.0%; Score 388.5; DB 5; Length 282;

Best Local Similarity 34.4%; Pred. No. 9e-27; Matches 96; Conservative 53; Mismatches 87; Indels 43; Gaps 7;

QY 52 VSLVALTGNVAVLM-----LLGCRNRNNAVSIIYI-LT-VAADEFLSG 93
DB 9 ISPVGFVENGILMLLCEFTVYTHLSIADISLFC-----IFLSIDYALDYELSSG 60
QY 94 HIICSPRLININHPISKISIPWTFPPYIGLSMLSAISTERCLSIIMPTWICRRRYL 153
DB 61 H-----YYITVLSVTPFLFGYNTGLYLITAIISVERCLSVLPYWRCHRPKQ 108
QY 154 SSVMCVLMLALSLRSILEMWFCDPLFSGADSVWCETSPFITIAMVFLCVLCGSSVLV 213
DB 109 SALVCALLMLSLCIVTM-YVMCIDRPEESHSDCAVIFNALSFLVPTSSVSTIL 167
QY 214 LVRIILGSRKMPRLRYVITLTLVFLVLCGLPFGIOMALFSRIHLDKVLPCVHLVSI 273
DB 168 VVKIRKWTASHSSKLYIVIMVITLIFLIPAMPRLLYLRYEY---WST-FGNLHHSIL 223
QY 274 FLNALNSANPIIYFVGSFRORONRONTKLVLQALOD 312
DB 224 LFSITINSSANPIYFVGSSEKSKKFKESLKVILTRAFKD 262

RESULT 11

US-08-118-270-76
Sequence 76, Application US/08118270
Patent No. 5506384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESSES:
ADDRESSES: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-76

Query Match 19.5%; Score 344; DB 1; Length 298;

Best Local Similarity 31.3%; Pred. No. 8.4e-23; Matches 94; Conservative 58; Mismatches 114; Indels 34; Gaps 11;

QY 48 LTCIVSLVALTGNVAVLMMLGCRNRNNAVSIIY-LT-VAADEFLSGHIICSPRLINI 105
DB 8 LTLCLGLV---GNGLVLMFPGFSIKTTPSIYIYFLHISADDIYLFSAV---ILLNLM 61
QY 106 RHPISKI-----LSPWTFPPYIGLSMLSAISTERCLSIIMDIWYICRRPYLSSVMCV 159
DB 62 GTFGLSPFDYVRVRSIVGLTFPAGVSLLPALISIERCVSIFPMWYRRRPKLSAGVCA 121
QY 160 LMLALSLSILEMWFCDPLFSGADSVWCETSPFITIAMLVF-----LCVYLCGSSVLV 214
DB 122 LMLLFLVLSYINHYFC-LIGHERASGTACIMDISLIGLILFLFCPIWVLP-----IAL 176
QY 215 VRIILGSRKMPRL-RYVITLTLVFLVLCGLPFGIOMALFSRIHLDW--KVFCHVHLV 271
DB 177 LHVECARRRQNSAKNHLVLAIVSVFLVSSITGLIDWFLF-----WVQIRAPPEYV 230
QY 272 SIPLSALNSANPIIYFVGSFRORONRONTKLVLQALODPEVDEGGGMLPQD-TLEL 330
DB 231 RDLICINSAKPIYVFIAGRDSQRLMEPLRVVFORALRDGAEPDDAASSTENTVTMEM 290

RESULT 12

PCT-US93-08528-76
Sequence 76, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESSES:
ADDRESSES: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-76

Query Match 19.5% Score 344; DB 5; Length 298;

Best Local Similarity 31.3% Pred No. 8,4e-23; Indels 34; Gaps 11;
Matches 94; Conservative 58; Mismatches 114;

QY 48 LCTIVSLVATLGNVAVLMLGCRMRNNAVSIIYI--LNLVAADFLPSGHIIICSPRLINI 105
DB 8 LILCGGLV---GNGVLWLPFGSIRKTPPSIYIFLHLSADGIVLFSKAV---IALNM 61
QY 106 RHPISKI-----LSPVWTFPPYFGLSMLSAISTERCUSTLMPYTHCRPRYLSSWCV 159
DB 62 GTFPGSPDYRRVRSRIVGLTFPGVSLPLPAISIRCVSVIPPMYWRRLSAGVCA 121
QY 160 LLMALSLRLSILEMWFCDPLFGSADSVWCETSDFTITMLVF-----LCVVLGSSVLV 214
DB 122 LLMALSLFLVYIHNFTC-LLGHEASGTACLANDISLGLIFLPCPIWVLPF---IAL 176
QY 215 VRLIGSRKMLPT-RLVYVITLTLVFLVFLGSLPFGIOWALFSRHLDM--KYLFGCHVLY 271
DB 177 LHVCRARRRQSAKLNNVLAIVSVFLVSSLYLGIDWLF-----WVFGIAPPEPV 230
QY 272 SIPLSALNSANPIIYFVFGSFRORONRMLKVLQRALQDTPVEDEGGMLPQE-TLEL 330
DB 231 RDLICINSSAKPIYVFTAGRDKSQRLWEPLRVFORALRDGAEGBDASSTPNTVTMEM 290

RESULT 13

US-08-981-825-6
Sequence 6, Application US/08981825
Patent No. 6040426
GENERAL INFORMATION:
APPLICANT: OGAWA, KAZUYAUKI
APPLICANT: TANAKA, KAZUYA
APPLICANT: NAGATA, KINYA
APPLICANT: TAKANO, SYOICHI
TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
TITLE OF INVENTION: TN2, GENE (B19) ENCODING THE SAME, AND
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,825

FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: MSHIM4.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-981-825-6

Query Match 14.5% Score 255.5; DB 3; Length 395;

Best Local Similarity 25.9% Pred No. 8e-15; Indels 75; Gaps 10;
Matches 83; Conservative 56; Mismatches 107;

QY 51 IVSIVATLGNVAVLMLGCRMRNNAVSIIYI--LNLVAADFL-----ELG-----G 93
DB 41 LSLILGLVNGVILFVVGCRMRQVTVTTVHLNLSLSDLSASLPPFTYFLAVGHSWELG 100
QY 94 HICSPPLNIRRPISKILSPVWTFPPYFGLSMLSAISTERCUSTLMPYTHCRPRYL 153
DB 101 TTFC-----KLHSSIFPLNMFASGFLSASISDRCLQVVRPWAQNHRTVAA 147
QY 154 SSWCVLLMALSLRLSILEMWFCDPLFGSADSVWC-----E 189
DB 148 AKKVLVLMALVAVNTVYFVRFTIRSDRIGICYNVLLNPGPRDRTCSROALA 207
QY 190 TSDPTITMLVFLCVLGGSLVLLVRLCGSRMPRLRLVYVITLTLVFLVFLGSLPFGI 249
DB 208 VSKFL-LAFVFLPLAIIASHAAVSL-RLQHRGRRP-GRFVRLVAVAVAFALCWGPGYHV 264
QY 250 QMALFSRTH-----LDMKVLFGCHVLSIFLSAL--NSSANPIIYFVFGSFRORONR 299
DB 265 PSLEARAHANPGRPLVWRGL-----PFTSLAFNSVANPVLVYLTCPDMLRKL 316
QY 300 QNLKVLQRALQDTPVEDEGG 320
DB 317 RSLRTVLESVLVDSELGAG 337

RESULT 14

US-09-480-784-6
Sequence 6, Application US/09480784
Patent No. 6166186
GENERAL INFORMATION:
APPLICANT: OGAWA, KAZUYAUKI
APPLICANT: TANAKA, KAZUYA
APPLICANT: NAGATA, KINYA
APPLICANT: TAKANO, SYOICHI
TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
TITLE OF INVENTION: TN2, GENE (B19) ENCODING THE SAME, AND
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/480,784
FILING DATE: 10-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,825
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: MSHIM4.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-480-784-6

Query Match 14.5%; Score 255.5; DB 3; Length 395;
Best Local Similarity 25.9%; Pred. No. 8e-15;
Matches 83; Conservative 56; Mismatches 107; Indels 75; Gaps 10;

51 IIVSLVATGNAVVLMLGCGRRRAVSIIYILNVAADPL-----PLS-----G 93
41 LADLIGLVGVGLFVVGCMRGQVTVTWLHLALSLSLASISPFPTTYFLAGHSWELG 100
94 HIICSPRLINIRHPSKILSPVTPPYTGLSMLSAISTERCLSLMPYWHCRBRPL 153
101 TTRC-----KHSIFFLMFPASGFLLSISLDRCLQVVRPWAQNHRTVA 147
154 SSWVCVLVLAISLRSILEMFCDFLFGSGADSVWC-----E 189
148 AHVVCVLAIVLAVNTVYFVRDTISRLDGRIMCYNVLLNPGDPDRATCNSROALA 207
190 TSDPITAMVPLCVVLGSSVLVLRILGSRKMPRLTLVTLTLVFLVFLGSLPGI 249
208 VSKFL-LAFLVPLAIISSHAASL-RLQRRGRRP-GRFVRLVAANVAAPALCWGPFYH 264
250 QMALFSRIH-----LDMKVLFCVHVLVSIPLSAL--NSSANPIYFVSGFRORNR 299
265 FSLLEAAAHANPGLRPLVWRL-----PFTVSLAFNFSVANPVLVYLTCPDMLKLR 316
300 QNLKLVQLRALQTPPEVDEGG 320
317 RSLRTVLESVLVDSEELGAG 337
Db

RESULT 15
US-07-759-568-2
Sequence 2, Application US/07759568
Patent No. 5374506
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
TITLE OF INVENTION: Human Interleukin-8 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSES: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759,568
FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS/5683/91535/WEH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 cusp
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-759-568-2

Query Match 13.4%; Score 235.5; DB 1; Length 354;
Best Local Similarity 28.9%; Pred. No. 4.2e-13;
Matches 94; Conservative 53; Mismatches 121; Indels 57; Gaps 16;

25 TELTPINGREBTPC--YKQTLG---FTGLTCIVSLVALTGA-VVIMLLGCMRRRAVSI 78
23 TGMPPVE-KDYSBCLVWTQTLNKVVVYVAVLFLSLGNSLVMVLVLYRSRNSVTDV 81
79 YILNVAADPLFISGHITCSPL--RLINIRHPSKILSPVTPPYTGLSMLSAISTERC 136
82 YILNLMAP-AFCPDHAYLGRLOGKRLDPRTPCKVSVLKEVNFYSGILLACISVDY 140
137 LSLMPPIWHCRBRPLISSVVCVLVLAISLRSILEMFCDFLFGSGADSVWC-ETSDPT 195
141 LAIVQST-RLTYOKRLVYFCIGVWLSLISLPFLRQVSPNNSSPVCEYEDGHNT 199
196 IAWLVELCVTL-----CGSSVLVLRILC-GSRKMPRLVYV-----TLLVTVLF 240
200 AKV-----CWLRLILPHTFGILPLVLMFCYGTTLRTLFQAHMGQGRAMRVFAVLLP 255
241 LILGLPFG-----IOMALFSRIHDMKVLFCVHVLVSIPLSALNSSANPIY 267
256 LILCMLPYNLVLADTLMRTHVIOETCORRELDRLADATEI-----LGLFLHCLNPITY 309
288 FVVGSPFRORONR--LKLVLQAL 310
310 AFIG-----ONFRNGFLKMLAARGL 329
Db

Search completed: October 27, 2004, 08:34:18
Job time: 41 secs

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OM protein - protein search, using sw model

Run on: October 27, 2004, 08:25:18 ; Search time 39 Seconds

(without alignments)
831.412 Million cell updates/sec

Title: US-09-867-570-2

Perfect score: 1763

Sequence: 1 MESKSSWVIRLIGFLSMDSTI.....EGCGWLPGQTLRLSGRLAQ 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	26.1	378	A39485	transforming prote
2	446.5	25.3	324	1 TVRTAS	transforming prote
3	430.5	24.4	325	1 TVHUS	transforming prote
4	428.5	24.3	324	2 S51001	transforming prote
5	371	21.0	343	2 A35639	G protein-coupled
6	240	13.6	355	2 JQ1231	interleukin-8 rece
7	238	13.5	353	2 A42009	PLMP-related recep
8	235.5	13.4	354	2 A23669	interleukin-8 rece
9	226.5	12.8	360	2 A53611	interleukin-8 rece
10	220	12.5	358	2 A53752	interleukin-8 rece
11	219.5	12.5	369	2 A41795	somatostatin recep
12	219.5	12.5	369	2 A45291	somatostatin recep
13	217	12.3	351	2 B42009	PLMP-related recep
14	214.5	12.2	346	2 S29248	somatostatin recep
15	214.5	12.2	388	2 JN0605	somatostatin recep
16	210	11.9	473	2 JCS835	anaphylatoxin C3a
17	209.5	11.9	363	2 I57940	somatostatin recep
18	209	11.9	356	2 S42066	interleukin-8 rece
19	206.5	11.7	364	2 A47249	brain-specific som
20	206	11.7	369	2 JQ2083	somatostatin recep
21	206	11.7	380	2 S36143	kappa opioid recep
22	205.5	11.7	355	2 A55733	G protein-coupled
23	205	11.6	333	2 I65989	G protein-coupled
24	204	11.6	380	2 A48227	kappa opioid recep
25	201.5	11.4	380	2 A55259	kappa opioid recep
26	201	11.4	352	2 A46520	N-formyl peptide r
27	201	11.4	380	2 JQ2434	kappa opioid recep
28	199	11.3	369	2 B41795	somatostatin recep
29	198.5	11.3	380	2 JQ2338	kappa opioid recep

30	196.5	11.1	350	1 A37963	complement C5a ana
31	196.5	11.1	371	2 JC5498	G protein-coupled
32	196.5	11.1	504	2 A41783	tachykinin recepto
33	196	11.1	384	2 JC4629	somatostatin recep
34	194.5	11.0	350	2 A39445	interleukin-8 rece
35	194	11.0	363	2 I57955	somatostatin recep
36	194	11.0	364	2 JN0763	somatostatin recep
37	193.5	11.0	375	2 JC5069	G protein-coupled
38	193	10.9	364	2 A49542	N-formyl peptide c
39	189	10.7	392	2 S65693	opioid receptor mu
40	188	10.7	359	2 I49341	MIP-1 alpha recept
41	187.5	10.6	352	1 S27357	complement C5a ana
42	187	10.6	340	2 JC7695	G protein-coupled
43	187	10.6	378	2 A55735	G protein-coupled
44	186	10.6	391	2 A41795	somatostatin recep
45	186	10.6	391	2 C41795	somatostatin recep

ALIGNMENTS

RESULT 1

A39485 transforming protein (mxg) - human

C/Species: Homo sapiens (man)

C/Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C/Accession: A39485

R/Komoc, C.; Weber, V.; Stimmakre, J.; Bihoreau, C.; Teutsch, B.; Corvol, P.; Clauser, Mol. Endocrinol. 5, 1477-1487, 1991

A/Title: Cloning and functional characterization of a novel mas-related gene, modulating

A/Reference number: A39485; MUID:92130997; PMID:1723144

A/Accession: A39485

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-378 <MON>

A/Cross-references: UNIPROT:P35410; GB:S78653; NID:G244209; PIDN:AAB21255.1; PID:G244210

A/Superfamily: mas transforming protein

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.1%; Score 461; DB 2; Length 378;

Best Local Similarity 37.9%; Pred. No. 2.7e-31;

Matches 107; Conservative 56; Mismatches 81; Indels 38; Gaps 10;

QY	51	IVSLVLTGNVAVLMLGCMRRNVAISITLNLVAADFLPSGHILCSPLRLINR----	106
DB	84	LVSLGVLNGVFWMLCCG-ATNPYVYTLHLVADVYTL-----CSAVGFLOYTLTLTY	138
QY	107	HPI-----SKLSPVTPPEYFGSLMSAISTERCLSTLMPYHCRPRYLSSVWCV	159
DB	139	HGVVFLIPDFLALISF---FSFVCLCLVAISTERCVLPYWRGHRPKYSNVCT	195
QY	160	LVNALSLRSILEWMPDFLPSGADSVWCETSD--PITLAWL--VLCCVLCSSLYVL	214
DB	196	LWGLPFCINIVKSLFLTY-----WKHVKAQVIFLKLSGFHALISLVCSSLYTL	247
QY	215	VRILCSRKMLPRLVYTLTLVLVPLLCGLPBGIOALPSRLHLDKVLFCVHLVSI	274
DB	248	IRFLCSGQOQKARIVAVVOISAPWFLMLAPSV-----APLTTDKMVTTSYLSL	302
QY	275	LSALNSSANPIIYFVSGFRQQRQNLKVLQALADTPREV	316
DB	303	L-IINSANPIIYFVSGSLKKRLKESLRLVILQALADKREV	343

RESULT 2

transforming protein mas - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004

C/Accession: A31816

R/Young, D.; O'Neill, K.; Jessell, T.; Wigler, M.

Proc. Natl. Acad. Sci. U.S.A. 85, 5339-5342, 1988

A/Title: Characterization of the rat mas oncogene and its high-level expression in the h

Db 272 SSANPFIYFVSGSSKKRFRSLKVLVTRAFKDEMQRROENG 315

RESULT 5

A:35639 G protein-coupled receptor RTA - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C/Accession: A35639

R:Kobay, P.C.; Figliet, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Marcus, D.R.; Lynch, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990

A>Title: RTA, a candidate G protein-coupled receptor: Cloning, sequencing, and tissue di

A/Reference number: A35639; MUID:90222168; PMID:2109324

A/Accession: A35639

A:Molecule type: mRNA

A/Residues: 1-343 <ROS>

A/Cross-references: UNIPROT:P23749; GB:M35297; NID:G206809; PID:AAA42087.1; PID:G206810

C:Superfamily: mas transforming protein

C/Keywords: G protein-coupled receptor; glycoprotein; membrane protein

F/4/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 21.0%; Score 371; DB 2; Length 343;
Best Local Similarity 33.1%; Pred. No. 9e-24;
Matches 99; Conservative 58; Mismatches 110; Indels 32; Gaps 11;

QY 48 LFCIVSLVATGNVAVLMLGCGMRRAVSVITLNLVAADFLSGHIICSPLELNIIR- 106

Db 53 LCLCLGLV---GGLVLMFPGFSGFKTPFSIFLHLASADGIYLFSAV---IALLMNGT 106

QY 107 -----HPISKILSPVMTFPYFIFGLSMLSAISTERCLSIPIWYHCRPRYLSVM 157

Db 107 FLGSPDYVRVRRVRIQ-LCTP--FAGVSLIPAIISIRCVSVIFPMYWRRRPRLSAGV 163

QY 158 CVLLMALSLRLSILEMFCDFLFGSADSVWCETSDFTIAMLVF--LCVVLGSSLVLLV 215

Db 164 CALLMLSLFLVTSIHNYFCMFLGHEASGTACLMMND-ISTGILFLFLCPLMLVFCIALIL 222

QY 216 RLICGSRKMLT-RLVYTTILLTVLVLCLGPRGIONALSRHLDK--KVLPGHVLVS 272

Db 223 HVCRRARRRORSAKLNHVLAIVSVFLVSSIVGIDIMFLP-----VFPQIPADPPRYVT 276

QY 273 IFSLALNSANPFIYFVSGSFRORQRONKQLVQLRALQDTPVEDSGGMLPQE-TLEL 330

Db 277 DLCTCNSSAKPIVYFLAGRDQGRMLERLVFQRALRGABRGDAASSTPNVTMEM 335

RESULT 6

JQ1231

interleukin-8 receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C/Accession: JQ1231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlowsky, C.; Vandembos, T.; Price, V.; Lyman, S.; Gerard

Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A>Title: Molecular characterization of the interleukin-8 receptor.

A/Reference number: JQ1231; MUID:91378994; PMID:1898400

A/Accession: JQ1231

A:Molecule type: DNA

A/Residues: 1-355 <BEC>

A/Cross-references: UNIPROT:P21109; GB:M74240; NID:G165438; PID:AAA31375.1; PID:G165439

R:Lee, J.; Khang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A>Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.

A/Reference number: A46483; MUID:92148149; PMID:11737938

A/Accession: A46483

A/Status: preliminary

A:Molecule type: mRNA

A/Residues: 1-355 <LEB>

A/Cross-references: GB:M82873; NID:G165440; PID:AAA31376.1; PID:G165441

A/Experimental source: neutrophil

A/Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:P.81530)

C:Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 13.6%; Score 240; DB 2; Length 355;
Best Local Similarity 27.4%; Pred. No. 9.4e-13;
Matches 92; Conservative 57; Mismatches 109; Indels 78; Gaps 17;

QY 25 TELPIINGREBTPC--YKQTLA---FTGLTCIVSLVATGNA-VLWMLGCGMRRAVSVI 78

Db 23 TGMPEPVE-KQYSPCLVVTQTLNKVVVIVAVLFLSLNSLVMLVILVSRNSRVTDV 81

QY 79 YILNLVAADFLFLSGHIICSPRLIN-----IRHPSKILSPVMTFPYFGLSMLSAIS 132

Db 82 YLNLMAAADLFL-----ALTPRIMAVSSEKGMIRGTPCLKXVSLVKEVNFSGIILLACIS 137

QY 133 TERCLSTLMPDWYHCR-----PRYLSVMCVLMAALSLRLSILEMFCDFLFGSADSVWC 188

Db 138 VDRYLAIV-----HATTLTQKRLHVFCILGIALSLISLPFLPRQVSPNNSSPVC 192

QY 189 -ETSDFITIAMLVFLCVV--LCGSSLVLVRIIC-GSRKMPRLVY-----TILLT 236

Db 193 YEDLGHTAKRMVRLRLPHTFGRIPLVLVLFYGFTRLRLFGAHNGQKRAMRVIFAV 252

QY 237 VLVFLCLGPFPGIOMALFSRIHLDKVLFC---HNLV-----SIFLS 276

Db 253 VLIPLCLMLPYNL-----VLADDTLKRTHVIGETCCRRNDIDRALDATEILG 299

QY 277 ALNSANPFIYFVSGSFRORQRONK--LKLVLORAL 310

Db 300 FLHSCNLPITYAFIG-----QNRNGFLKMLAARGL 330

RESULT 7

C42009

FMPL-related receptor 2 - human

N/Alternate names: FMPL-related receptor 1; probable chemotactic receptor FPRH2

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: C42009

R:Boo, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.

Genomics 13, 437-440, 1992

A>Title: Mapping of genes for the human C5a receptor (C5AR), human FMPL receptor (FPR),

A/Reference number: A42009; MUID:92307681; PMID:1612600

A/Accession: C42009

A/Status: nucleic acid sequence not shown

A:Molecule type: DNA

A/Residues: 1-353 <BNO>

A/Cross-references: UNIPROT:P25089; GB:M76673; NID:G182668; PID:G182669

C/Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known, appears nc

C/Genetics:

A/Gene: GDB:FPRL2

A/Cross-references: GDB:128855; OMIM:136539

A/Map position: 19q13.3-19q13.4

A/Intons: #status absent

C:Superfamily: vertebrate rhodopsin

C/Keywords: Chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 13.5%; Score 238; DB 2; Length 353;
Best Local Similarity 23.8%; Pred. No. 1.4e-12;
Matches 81; Conservative 76; Mismatches 112; Indels 72; Gaps 15;

QY 29 PINGREB-----TPCYQTLSTFTGLTCIVSLVATGNAVVLMLGCGMRRAVSVIYI 80

Db 8 PLMBTEFVLPBPAGHTVLMIFSLVHGVTVPGL---GGLVIVWAGFRTTRVNTICY 64

QY 81 LNLVAADFLFLSGHIICSPRLINI---RHP-----ISKILSPVMTFPYFGLSMLSAIS 132

Db 65 LNLVAADFLFSFA---ILPFRMVSVAREKMPFASCKVHVWIDINLFPVSVYLITIA 120

QY 133 TERCLSTLMPDWYHCRPRYLSVMCVLMAALSLRLSILEMFCDFLFGSADSVWC 180

Db 121 LDRCTCVLHPAMQNHRTMSLAKRVMTGLMIFITVLLPNFIPTTISTTGDTYCLFNF 180

QY 181 SGADSVWCET-----SDFITIAMLVFLCVVLCGSSLVLVRIIC-----G 220

Db 181 ----AFMGDTAVERLNVETMAKVELLHFIIGTVPMSIITVCYGIINAKIRHNMKS 236
 QY 221 SRKMPRLRYVLTITLVVFLICGPF---GIQWALFSR---IHLDMKVLFGVHLVSI 274
 Db 237 SR--PL-RVFAAV---VASFTICWPFYEIGILMAWMLKEMLNKIKIILVILNPTS-S 289
 QY 275 LSAINSSANPIITYFVSGFRORONRLKLVIALODTPE 315
 Db 290 LAFNNSCLNPILYVFMGRNFORLIRSLPTSLEALTEVPD 330

RESULT 8

A23669
 Interleukin-8 receptor, high affinity - rabbit

N:Alternate names: FMLP receptor

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C/Accession: A23669

R/Thomas, K.M.; Pyun, H.Y.; Navarro, J.

J. Biol. Chem. 265, 20061-20064, 1990

A>Title: Molecular cloning of the Fmet-leu-Phe receptor from neutrophils.

A/Reference number: A23669; MUID:91056034; PMID:1700779

A/Accession: A23669

A/Molecule type: mRNA

A/Residues: 1-354 <THO>

A/Cross-references: UNIPROT:P21109; GB:M58021; GB:J05705; NID:g165442; PIDN:AAA1377.1;

C:Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 13.4%; Score 235.5; DB 2; Length 354;

Best Local Similarity 28.9%; Pred. No. 2.2e-12;

Matches 94; Conservative 53; Mismatches 121; Indels 57; Gaps 16;

QY 25 TELPINGERETPC--YKOTLS---FTGLTCVSLVALTGNA-VVLMILGCMRRNAVS 78
 Db 23 TGMPEVH-KDYSPLCVTQTLNKYVVVYVALVFLSLGSLVMLVILYSSNSVTDV 81
 QY 79 YIINLVADFLPLSGHIIICSP--RLINI RHPISKILSPWTFPFYIGLSMLSAISTERC 136
 Db 82 YLNLINLAAP-AFCPDHATVGRLOGRKDPRTPLCKVSVLKEVNPYSGILLACISYDXY 140
 QY 137 LSLIMPIWYHCRPRYLSVWCVLLMALSLRSILEMFCDFLFGADSVWC-ETSDPT 195
 Db 141 LAIVQST-RTLTQKHILVAFICLGIWALSLILSPFLFRQVSPNNSPVCYEDIGHNT 199
 QY 196 IAWLVFICVVL-----GSSSLVILVRLIC-GSRKMPULRLV-----TILTVAF 240
 Db 200 AKM---CMVLRILPHRTGFLPLVLMFCYGFTRTLFQAMGQKRAMRVIFAVVLF 255
 QY 241 LLCGLPFG-----IQWALFSRIHLDKVLFGVHLVSIPLSALNSSANPIIY 287
 Db 256 LLCGLPYNLVLLADTLKRTVYIQTCCQRNELDRALDATEI-----LGFSLCLNPITY 309
 QY 288 FVVGSRORONRL--LKVIALORAL 310
 Db 310 AFIG-----QMFRRGFLKMLAARGL 329

RESULT 9

A53611

Interleukin-8 receptor type B - human

C/Species: Homo sapiens (man)

C>Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C/Accession: I37898; I38712; A53611; A39446

R/Hubaj, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 265, 26381-26389, 1994

A>Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type B.

A/Accession: I37898

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-360 <RBS>
 A/Cross-references: UNIPROT:P25025; EMBL:U11869; NID:g511801; PIDN:AA6065.1; PID:g5118

A/Accession: I38712
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-15 <RE2>
 A/Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA4380.1; PID:g511809; EMBL:U11873;
 I1876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NID
 J. Biol. Chem. 269, 11065-11072, 1994
 A>Title: Structure, genomic organization, and expression of the human interleukin-8 recep
 A/Reference number: A53611; MUID:94209273; PMID:7512557

A/Accession: A53611

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 6-360 <SPR>

A/Cross-references: GB:M99412; GB:I19593

R/Murphy, P.M.; Tiffany, H.L.

Science 253, 1280-1283, 1991

A>Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor

A/Reference number: A39446

A/Accession: A39446

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 6-360 <MUR>

A/Cross-references: GB:M73969

C/Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, inc

C/Genetics:

A/Map position: 2q35-2q35

C:Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.8%; Score 226.5; DB 2; Length 360;

Best Local Similarity 26.3%; Pred. No. 1.3e-11;

Matches 82; Conservative 52; Mismatches 103; Indels 75; Gaps 13;

QY 34 EETPCYKOTLSFTG-----LTCISLVALTGNA-VVLMILGCMRRNAVSIIINLVAD 87
 Db 35 DAAPCEPSLEINKYFVYIYVALVFLSLGSLVMLVILYSSNSVTDVYLLNLAD 94
 QY 88 PLF-----LSGHIIICSPRLNIRHPIKILSPWTFPFYIGLSMLSAIS 132
 Db 95 LILFALTPLIWAASKVNGMIFGFLC-----KVSLSLKEVNFYSIGILLACTS 141
 QY 133 TERCLSLPIWYHCR---PRYSVWCVLLMALSLRSILEMFCDFLFGADSVWC 188
 Db 142 VDRYLAIV-----HATRLTLQKRYLVKFCISIMGLSILLALPVLLFRITYSSNVSPAC 196
 QY 189 -ETSDPTIAMLVPLCVL--LCGSSLVILVRLIC-GSRKMPULRLV-----TILTV 236
 Db 197 YEDMGNNNTANWMLRLIRLPQSGFIVPLILMFCYGFTRTLFKAMGQKRAMRVIFAV 256
 QY 237 VLVFLICGLPFG-----IQWALFSRIHLDKVLFGVHLVSIPLSALNSSAN 283
 Db 257 VILFLLCMLPYNLVLLADTLKRTVYIQTCCQRNHIDRALDATEI-----LGFSLCLN 310
 QY 284 PIIVFVVG-SFR 294
 Db 311 PLIYAFIQGKFR 322

RESULT 10

A53752

Interleukin-8 receptor (clone 5B1a) - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: A53752

R/Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro

J. Biol. Chem. 269, 12391-12394, 1994

A>Title: Molecular characterization of a novel rabbit interleukin-8 receptor isoform.

A/Reference number: A53752; MUID:94230294; PMID:8175642

A/Accession: A53752

A/Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-358 <PRA>
 A:Cross-references: UNIPROT:P35344; GB:I24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.5%; Score 220; DB 2; Length 358;
 Best Local Similarity 26.5%; Pred. No. 4,5e-11;
 Matches 84; Conservative 53; Mismatches 112; Indels 68; Gaps 14;

QY 25 TELPPIINGREBPCYKQTLSTFTGLTCIVS-----LVALTGNA-VVIMLCCGRMRNAVSI 78
 DB 25 TDLPP-TLDSAPCRSRSLSTNSVYVILYIVLFLSLGNSLVMLVILYSRSTCVTDV 83
 QY 79 YIINLVADPLFLSGHICGPRILINIRH-----PISKLSPTMTPTPTIGLSMLSAIS 132
 DB 84 YIINLVADPLFLSGHICGPRILINIRH-----PISKLSPTMTPTPTIGLSMLSAIS 139
 QY 133 TERCLSTLMPDWCR-----PRYLSVMCVLMLALSLRSILEMFCDFLFGSGADSVWC 188
 DB 140 VDRYLAIV-----HATTTMIOKRLVYFCLSMGVSLIISPLIFRNALFPNNSPVC 194
 QY 189 -ETSDPTITAMVFLCVV--LCGSSVLVLRILC-----GSRKMPITRLYVT 232
 DB 195 YEDMGNSSTAKRMYRLPQTFPFIPLVLMFCVYFTLRTLPQAHMGQKH---RAMRV 250
 QY 233 ILITVLVPLLCGLPFGICQMLFSRIHLDKVLFCYVHL-----VSIFLSAL 278
 DB 251 IFVAVVLFLLCWLPLYNL-----VLLTDLTMRTHVIOETCERNRIDALDATEILGFL 303
 QY 279 NSSANPIYFVGV-SFR 294
 DB 304 HSCLNPIIYAFIGQKFR 320

RESULT 11

41795
 somatostatin receptor 2 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
 C/Accession: D41795; I56236
 R/Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Saito, S.
 Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
 A>Title: Cloning and functional characterization of a family of human and mouse somatostatin receptor number: A41795; MUID:92106031; PMID:1346068
 A:Reference number: A41795
 A:Accession: D41795
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-369 <YAM>
 A:Cross-references: UNIPROT:P30875; GB:M61832; NID:g201060; PIDN:AAA58256.1; PID:g201061
 R/Ellicott, D.B.; Metwalli, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.V.
 J. Immunol. 153, 1180-1186, 1994
 A>Title: T lymphocytes isolated from the hepatic granulomas of schistosome-infected mice
 A:Reference number: I56236; MUID:94300079; PMID:7913111
 A:Accession: I56236
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 99-309 <RES>
 A:Cross-references: GB:G71756; NID:g560631
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 12.5%; Score 219.5; DB 2; Length 369;
 Best Local Similarity 28.3%; Pred. No. 5.1e-11;
 Matches 95; Conservative 55; Mismatches 131; Indels 55; Gaps 18;
 QY 23 LGTELPIINGREB-PCYKQTLSTFTGLTCIVSLVLTGNAVLM-LICGRMRNAVSI 78
 DB 21 LNSGLSGNSNGTEPYDNTSNVLFYFVVCVGLCGNTLYIVILRYAKKKTITNI 80
 QY 79 YIINLVADPLFLSGHICGPRILINIRHPIK-ILSPVMT---FPYFGLSMLSAISTE 134
 DB 81 YIINLVADPLFLSGHICGPRILINIRHPIK-ILSPVMT---FPYFGLSMLSAISTE 139

QY 135 RCLSTLMPI-----MYHCRPRYLSVWCYVLMALSLRSILEMFCDFLFGSGADSVWC 177
 DB 140 RYLAIVHPIKSAK---RRPR-TAKMINAVWCVSL-VLPIIMYAGLSNMGRESSCT 194
 QY 178 FLFGADSVWCETSDPTITAMVFLCV---VLCSSVLVLR-----ILGSRMPITRL 229
 DB 195 INMPGESGAM-YTGFIYAFILGFLVPLTILICLYFIILIKVSGGIRVSSGRKRSK 252
 QY 230 YVT-ILITVLVPLLCGLP-----GIQWALFSRIHLDKVLFCYVHLVSLFSLANSS 281
 DB 253 KVTSMVSIIVAVPIFCWLPFYIFNVSSVSAISPTPAL--KGMDFV---VILTYANSC 306
 QY 282 ANPIYFVGVFRORONRNLKVLQRALQDTPEVD 317
 DB 307 ANPIYAFSLDNFKKSFQNVLCIVKVSCTEDGRSD 342

RESULT 12

445291
 somatostatin receptor, somatotropin release-inhibiting factor receptor, SRIF receptor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 25-Mar-1993 #sequence revision 18-Nov-1994 #text change 09-Jul-2004
 C/Accession: A45291
 R/Kluxen, F.W.; Bruns, C.; Lubbert, H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4618-4622, 1992
 A>Title: Expression cloning of a rat brain somatostatin receptor cDNA.
 A:Reference number: A45291; MUID:92262491; PMID:1374909
 A:Accession: A45291
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-369 <KLX>
 A:Cross-references: UNIPROT:P30680; GB:M93273; NID:g207026; PIDN:AAA42165.1; PID:g207027
 A>Note: Sequence extracted from NCBI backbone (NCBI:102315, NCBI:102316)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.5%; Score 219.5; DB 2; Length 369;
 Best Local Similarity 28.3%; Pred. No. 5.1e-11;
 Matches 95; Conservative 55; Mismatches 131; Indels 55; Gaps 18;

QY 23 LGTELPIINGREB-PCYKQTLSTFTGLTCIVSLVLTGNAVLM-LICGRMRNAVSI 78
 DB 21 LNSGLSGNSNGTEPYDNTSNVLFYFVVCVGLCGNTLYIVILRYAKKKTITNI 80
 QY 79 YIINLVADPLFLSGHICGPRILINIRHPIK-ILSPVMT---FPYFGLSMLSAISTE 134
 DB 81 YIINLVADPLFLSGHICGPRILINIRHPIK-ILSPVMT---FPYFGLSMLSAISTE 139
 QY 135 RCLSTLMPI-----MYHCRPRYLSVWCYVLMALSLRSILEMFCDFLFGSGADSVWC 177
 DB 140 RYLAIVHPIKSAK---RRPR-TAKMINAVWCVSL-VLPIIMYAGLSNMGRESSCT 194
 QY 178 FLFGADSVWCETSDPTITAMVFLCV---VLCSSVLVLR-----ILGSRMPITRL 229
 DB 195 INMPGESGAM-YTGFIYAFILGFLVPLTILICLYFIILIKVSGGIRVSSGRKRSK 252
 QY 230 YVT-ILITVLVPLLCGLP-----GIQWALFSRIHLDKVLFCYVHLVSLFSLANSS 281
 DB 253 KVTSMVSIIVAVPIFCWLPFYIFNVSSVSAISPTPAL--KGMDFV---VILTYANSC 306
 QY 282 ANPIYFVGVFRORONRNLKVLQRALQDTPEVD 317
 DB 307 ANPIYAFSLDNFKKSFQNVLCIVKVSCTEDGRSD 342

RESULT 13

842009
 FMLP-related receptor 1 - human
 N/Alternate names: FMLP receptor homolog FPR2; formyl peptide receptor like-1; probable
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence revision 14-Jul-1995 #text change 09-Jul-2004
 C/Accession: B42009; JCI258; J01521; A42492; I54751; S21581

C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: UN0605; JN0762; A47457
R/Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A/Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A/Reference number: JN0605; MUID:9320656; PMID:8512564
A/Accession: JN0605
A/Molecule type: DNA
A/Residues: 1-388 <XUY>
A/Cross-references: UNIPROT:P31391; GB:J14856; NID:G22499; PIDN:AAA36623.1; PID:G292500
R/Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A/Title: Cloning, functional expression and pharmacological characterization of a fourth
A/Reference number: JN0762; MUID:93384611; PMID:8373420
A/Accession: JN0762
A/Molecule type: DNA
A/Residues: 1-388 <YAM>
A/Cross-references: GB:D16826; NID:9693907; PIDN:BA04106.1; PID:9693908
R/Robner, L.; Raulf, F.; Bruno, C.; Buetner, R.; Hofstaedter, F.; Schule, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A/Title: Cloning and characterization of a fourth human somatostatin receptor.
A/Reference number: A47457; MUID:93248256; PMID:8483934
A/Accession: A47457
A/Molecule type: DNA
A/Residues: 1-82, 'T', 84-364, 'K', 366-388 <ROH>
A/Cross-references: GB:J07833; NID:9307429; PIDN:AAA60565.1; PID:9307430
A/Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBI:P:130858)
C/Comment: This protein mediates the diverse actions of the tetradecapide somatostatin.
C/Genetics:
A/Gene: GDB:SSTR4
A/Cross-references: GDB:202662; OMIM:182454
A/Map position: 20p11.2-20p11.2
A/Intons: #status absent
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phc
F/47-73/Domain: transmembrane #status predicted <TM1>
F/84-109/Domain: transmembrane #status predicted <TM2>
F/121-142/Domain: transmembrane #status predicted <TM3>
F/162-184/Domain: transmembrane #status predicted <TM4>
F/208-238/Domain: transmembrane #status predicted <TM5>
F/257-284/Domain: transmembrane #status predicted <TM6>
F/291-314/Domain: transmembrane #status predicted <TM7>
F/24/Binding site: carbohydrate (asn) (covalent) #status predicted
F/119-198/Disulfide bonds: #status predicted
F/161,253/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pr
F/327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 12.2%; Score 214.5; DB 2; Length 388;
Best Local Similarity 25.9%; Pred. No. 1.4e-10; Indels 59; Gaps 14;
Matches 95; Conservative 61; Mismatches 152;

QY 14 LSNMSTIPVLGTE-----LTPNGREET--PCYKOTLSFTGLTCI---VSLV 55
DB 1 MSAPSTLPFGSGEGSLGTAWPSANASSAPAEAEAVAGPGDARAAGWVAIQCIYALVCLV 60
QY 56 ALTGNAVVM-LIGCRNRNAVSIYIINLVADPLF-LSGHIICSPLRLINRH-PISKI 112
DB 61 GLVGNALVIRVIAKMKATATNIIYLLNLAVDELFWLSVFPVASSAAL--RHMPGVS 117
QY 113 LS-----PVMTFFPIGSMLSAISTERCLSIIMPIWTHCRPRYLSVMCILLMALSLR 168
DB 118 LCRAVLSVDGLNMFTSVFCLIVLSVDKRYAVVHPLRAATYRRPSVACINIGVWLASLV 177
QY 169 SLEWMECDFL-FSGADSVNCE-----TSPFITAMLV-----FLCVVLG-----GS 209
DB 178 TLPIAFADTRPARGGQAVACNQPWPAASAVFVVVTFLLGLPLVLAIGLCYLLIVGK 237
QY 210 SLVLLVRIICGRKMPRLRLVYITLLTVLVFLGLGFPGIQWALFSRIHDMKVLFCVH 269
DB 238 MRAVALRAGWQORRRSEKKITRLVLMVVVFLCWMPEFYV---VQLINLVVTSLDATVN 293
QY 270 LVGIFLSALNNSNPITVFVGSFRQNRQNLKLVQRLALQDTPBVDEGGMLPQETLE 329

DB 294 HVELIISVANSKANPILYGLS-----DNFRRSFORVLCRCCLLBGAGAREEPD 345
QY 330 LSGSRLE 336
DB 346 YVATALK 352

Search completed: October 27, 2004, 08:35:03
Job time: 40 secs

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OM protein - protein search, using sw model

Run on: October 27, 2004, 08:24:12 ; Search time 190 Seconds

(without alignments)
1020.533 Million cell updates/sec

Title: US-09-867-570-2

Perfect score: 1763

Sequence: 1 MESKSSWVIRLGFSLMSDSTI.....EGGWLPGETLHLSGRLEQ 337

Scoring table: ELOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	95.7	322	1 MRG3_HUMAN	Q96LBO homo sapien
2	1663	94.3	322	1 AAH67292	AAH67292 homo sapi
3	1606	91.1	322	1 SNS2_HUMAN	Q8CDE0 homo sapien
4	1411	80.0	322	1 SNS3_HUMAN	Q8CDE0 homo sapien
5	1383	78.4	322	1 MRG1_HUMAN	Q96LBO homo sapien
6	1382	78.4	322	1 SNS5_HUMAN	Q8CDE0 homo sapien
7	1367	77.5	322	1 MRG4_HUMAN	Q96LBO homo sapien
8	989.5	56.1	330	2 MRG2_HUMAN	Q96LBO homo sapien
9	989.5	56.1	330	2 AAH63450	AAH63450 homo sapi
10	823.5	46.7	323	2 Q7TN42	Q7TN42 rattus norv
11	820.5	46.5	323	2 SNS1_RAT	Q8CDE0 rattus norv
12	797	45.2	322	2 Q8CDE0	Q8CDE0 rattus norv
13	782	44.4	304	1 MRGA_RAT	Q7TN42 rattus norv
14	778	44.1	331	2 Q91YB7	Q91YB7 rattus norv
15	763	43.3	338	2 Q8CDE4	Q8CDE4 mus musculu
16	763	43.3	338	2 Q91ZC2	Q91ZC2 mus musculu
17	761	43.2	304	1 MGAI_MOUSE	Q91ZC2 mus musculu
18	754	42.8	294	2 Q7TN48	Q7TN48 rattus norv
19	739.5	41.9	301	1 MGAE_MOUSE	Q91ZC2 mus musculu
20	729	41.3	302	1 MGAT_MOUSE	Q91ZC2 mus musculu
21	722.5	41.0	305	1 MGAT_MOUSE	Q91ZC2 mus musculu
22	713	40.4	321	2 Q91ZC0	Q91ZC0 mus musculu
23	703	39.9	338	2 Q91ZC3	Q91ZC3 mus musculu
24	691.5	39.2	333	1 MGAA_MOUSE	Q91ZC2 mus musculu
25	682.5	38.7	331	2 AAH6040	AAH6040 mus muscu
26	681.5	38.7	333	2 Q7TN45	Q7TN45 rattus norv
27	680.5	38.6	305	1 MGAT_MOUSE	Q91ZC2 mus musculu
28	680	38.6	304	1 MGAT_MOUSE	Q91ZC2 mus musculu
29	674	38.2	322	2 Q91ZB9	Q91ZB9 mus musculu
30	669.5	38.0	305	1 MGAB_MOUSE	Q91ZC2 mus musculu
31	638	36.2	314	2 Q7TN47	Q7TN47 rattus norv

32	626.5	35.5	353	2 Q7TN44	Q7TN44 rattus norv
33	617.5	35.0	312	2 Q91ZC1	Q91ZC1 mus musculu
34	596.5	33.8	328	2 Q7TN50	Q7TN50 rattus norv
35	578.5	32.8	245	2 Q7TN43	Q7TN43 rattus norv
36	576.5	32.7	247	2 Q7TN46	Q7TN46 rattus norv
37	568.5	32.2	330	2 Q7TN51	Q7TN51 mus musculu
38	541.5	30.7	320	1 MRGD_MACFA	Q61786 macaca fasc
39	541.5	30.7	320	1 MRGD_MACFA	Q61786 macaca fasc
40	506	28.7	321	1 MRGD_HUMAN	Q8CDE0 homo sapien
41	506	28.7	321	2 AAR05120	AAR05120 homo sapi
42	506	28.7	321	2 BAD20638	BAD20638 homo sapi
43	503	28.5	310	2 Q71119	Q71119 mus musculu
44	503	28.5	310	2 Q91ZB7	Q91ZB7 mus musculu
45	503	28.5	310	2 CAC86257	CAC86257 mus muscu

ALIGNMENTS

RESULT 1
MRG3_HUMAN STANDARD; PRT; 322 AA.
ID Q96LBO; Q8TDE1;
AC Q96LBO; Q8TDE1;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Mes-related G-protein coupled receptor member X3 (Sensory neuron-specific G-protein coupled receptor 1).
GN Name=MRG3; Synonym=SNR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11551509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of nociceptive sensory neurons."
RL Cell 106:619-632(2001).
RN [2]
RP SEQUENCE FROM N.A., VARIANT ASN-169, AND TISSUE SPECIFICITY.
RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nrn15;
RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O., Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M., Goesslin M., Fortin Y., Benaville D., Shen S., Stroem P., Payza K., Dray A., Walker P., Ahmad S.;
RT "Proenkephalin A gene products activate a new family of sensory neuron-specific GPCRs."
RL Nat. Neurosci. 5:201-209(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Stranberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F., Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Tohyuki S., Carninci P., Mullaly S.J., Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiyk S.W., Vallayon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schmechel J., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Mas subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AY042215; AAK91806.1; -
 DR EMBL: AF474987; AAL86878.2; -
 DR EMBL: BC067292; AAH67292.1; -
 DR MIM: 607229; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Polymorphism; Transmembrane.
 FT DOMAIN 1 31 Extracellular (Potential).
 FT TRANSSEM 32 52 1 (Potential).
 FT TRANSSEM 53 60 Cytoplasmic (Potential).
 FT TRANSSEM 61 81 2 (Potential).
 FT TRANSSEM 82 96 Extracellular (Potential).
 FT TRANSSEM 97 117 3 (Potential).
 FT TRANSSEM 118 140 Cytoplasmic (Potential).
 FT TRANSSEM 141 161 4 (Potential).
 FT TRANSSEM 162 177 Extracellular (Potential).
 FT TRANSSEM 178 198 5 (Potential).
 FT TRANSSEM 199 213 Cytoplasmic (Potential).
 FT TRANSSEM 214 234 6 (Potential).
 FT TRANSSEM 235 254 Extracellular (Potential).
 FT TRANSSEM 255 275 7 (Potential).
 FT TRANSSEM 276 322 Cytoplasmic (Potential).
 FT TRANSSEM 322 322 D -> N (in dbSNP:4274188).
 FT VARIANT 169 169 /FTID=VAR 019434.
 FT CONFLICT 3 3 S -> P (in Ref. 2).
 FT CONFLICT 82 82 C -> R (in Ref. 3).
 FT CONFLICT 307 307 W -> Q (in Ref. 3).
 FT CONFLICT 319 319 R -> K (in Ref. 2).
 KW VARIANT
 SQ SEQUENCE 322 AA; 36484 MW; 2531B8F0CB4EB74 CRC64;
 Query Match 95.7%; Score 1688; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 1.2e-115;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 RHLDWKVLPCHVHLVSLFSLANSSANPITYFVGSPFRONONKLVLPALQDTP 300
 QY 316 VDEGGWLPSTLELSSRLSQ 337
 DB 301 VDEGGWLPSTLELSSRLSQ 322
 RESULT 2
 AAH67292
 ID AAH67292 PRELIMINARY; PRT; 322 AA.
 AC AAH67292;
 DT 25-MAR-2004 (TRENDEL. 27, Created)
 DT 25-MAR-2004 (TRENDEL. 27, Last sequence update)
 DT 25-MAR-2004 (TRENDEL. 27, Last annotation update)
 DE G protein-coupled receptor MRG3.
 GN MRG3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RC MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.J., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uebli T.B., Toshlyuk S., Carninci P., Prange C., Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mulhany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton E., Kettelman M., Madan A., Rodriguez Y., Bouffard G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S., Krzywinski M.I., Skalska U., Smalton D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RC Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC067292; AAH67292.1; -
 KW Receptor.
 SQ SEQUENCE 322 AA; 36479 MW; B91DC082B6D95DA8 CRC64;
 Query Match 94.3%; Score 1663; DB 2; Length 322;
 Best Local Similarity 99.4%; Pred. No. 7.9e-114;
 Matches 320; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 256 RHLDWKVLFCHVHLVIFLSALNSSANPIYFVGSFRORONRMLKVLQALADTPE 315
 DB 241 RHLDWKVLFCHVHLVIFLSALNSSANPIYFVGSFRORONRMLKVLQALADTPE 300
 QY 316 VDEGGWMLPQETLELSSRLQ 337
 DB 301 VDEGGWMLPQETLELSSRLQ 322

RESULT 3
 SNS2_HUMAN STANDARD; PRT; 322 AA.
 AC Q8TDE0;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sensory neuron-specific G-protein coupled receptor 2.
 GN Name=SNRS2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/n815;
 RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
 RA Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
 RA Dray A., Walker P., Ahmad S.;
 RT "Proenkephalin A gene products activate a new family of sensory
 RT neuron-specific GPCRs";
 RL Nat. Neurosci. 5:201-209(2002).
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 CC nociceptive neurons. May regulate nociceptor function and/or
 CC development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 CC root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Mas subfamily.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: AF474988; AAL6879.2;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PFO0001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 32
 FT TRANSMEM 33 53
 FT DOMAIN 54 60
 FT TRANSMEM 61 81
 FT DOMAIN 82 96
 FT TRANSMEM 97 117
 FT DOMAIN 118 140
 FT TRANSMEM 141 161
 FT DOMAIN 162 177
 FT TRANSMEM 178 198
 FT DOMAIN 199 213
 FT TRANSMEM 214 234
 FT DOMAIN 235 254
 FT TRANSMEM 255 275
 FT DOMAIN 276 322

FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE - 322 AA; 36594 MW; D8C24308EB34611B CRC64;
 Query Match 91.1%; Score 1606; DB 1; Length 322;
 Best Local Similarity 96.0%; Pred. No. 1.2e-109;
 Matches 309; Conservative 4; Mismatches 9; Gaps 0;
 QY 16 MDSTIPVLTGELTPINGREETPCYKOTLSFTGTCIVSLVAGNAVLMILGCRMRNA 75
 DB 1 MDPTVPLVGLTLPINGREETPCYKOTLSFTGTCIVSLVAGNAVLMILGCRMRNA 60
 QY 76 VSIYIINLVADPLFLSGHILCSPLRLINIRHPSKILSPVMTPEFYIGLSAISTER 135
 DB 61 VSIYIINLVADPLFLSGHILCSPLRLINIRHPSKILSPVMTPEFYIGLSAISTER 120
 QY 136 CUSIIMPVYHCRPRYLSSVGVLLMALSLSLIEMWCDPLFGSADSVKETSFT 195
 DB 121 CUSIIMPVYHCRPRYLSSVGVLLMALSLSLIEMWCDPLFGSADSVKETSFT 180
 QY 196 IAWLVFVLCVVLGSSVLVLRILGSRKMP/LRYVYTLTLVAVFLCGPFGIOMALFS 255
 DB 181 IAWLVFVLCVVLGSSVLVLRILGSRKMP/LRYVYTLTLVAVFLCGPFGIOMALFS 240
 QY 256 RHLDWKVLFCHVHLVIFLSALNSSANPIYFVGSFRORONRMLKVLQALADTPE 315
 DB 241 RHLDWKVLFCHVHLVIFLSALNSSANPIYFVGSFRORONRMLKVLQALADTPE 300
 QY 316 VDEGGWMLPQETLELSSRLQ 337
 DB 301 VDEGGWMLPQETLELSSRLQ 322

RESULT 4
 SNS3_HUMAN STANDARD; PRT; 322 AA.
 AC Q8TDE0;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sensory neuron-specific G-protein coupled receptor 3.
 GN Name=SNRS3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/n815;
 RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
 RA Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
 RA Dray A., Walker P., Ahmad S.;
 RT "Proenkephalin A gene products activate a new family of sensory
 RT neuron-specific GPCRs";
 RL Nat. Neurosci. 5:201-209(2002).
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 CC nociceptive neurons. May regulate nociceptor function and/or
 CC development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins including BAM2 (bovine adrenal
 CC medulla peptide 22) and BAM (8-22). BAM2 is the most potent
 CC compound and evoked a large and dose-dependent release of
 CC intracellular calcium in stably transfected cells. G(alph)aq
 CC proteins are involved in the calcium-signaling pathway.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 CC root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Mas subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL, AF474989; AAL86880.2; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein, Transmembrane.
 FT DOMAIN 1 31
 FT TRANSMEM 32 52
 FT DOMAIN 53 67
 FT TRANSMEM 68 88
 FT DOMAIN 89 96
 FT TRANSMEM 97 117
 FT DOMAIN 118 144
 FT TRANSMEM 145 165
 FT DOMAIN 166 177
 FT TRANSMEM 178 198
 FT DOMAIN 199 221
 FT TRANSMEM 222 242
 FT DOMAIN 243 254
 FT TRANSMEM 255 275
 FT CARBOHYD 16
 SQ SEQUENCE 322 AA; 36287 MW; 4C43B33E5DCEBF5 CRC64;
 Query Match 80.0%; Score 1411; DB 1; Length 322;
 Best Local Similarity 84.5%; Pred. No. 2.2e-95;
 Matches 272; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

QY 16 MDSTIPVLTGTEPTINGREPTCYQKTLSPFGCTGIVSLVLTGNAVLTMLGCRMRNA 75
 DB 1 MDPTVSTLDTLTLINGTEFTCYKQTLSTLVTCIVSLVLTGNAVLTMLGCRMRNA 60
 QY 76 VSIYIILNVADFLSGHIIICSPRLINIRHPISKILSPVTPPYFTGLSMISAISTER 135
 DB 61 FSIYIILNVADFLSGHIIICSPRLINIRHPISKILSPVTPPYFTGLSMISAISTER 120
 QY 136 CLSLIMPIWHRCHPRRIYSSVACVLTMLSLRSLTLEMMFCDFLFGADSWCERSDPT 195
 DB 121 CLSLIMPIWHRCHPRRIYSSVACVLTMLSLRSLTLEMMFCDFLFGADSWCERSDPT 180
 QY 196 IAWLVFCVVLGSSSLVLTAVRILGSRKMPRLVTVTLTVLFGCLPFGIOWALFS 255
 DB 181 VAWLVFCVVLGSSSLVLTAVRILGSRKMPRLVTVTLTVLFGCLPFGIOWALFS 240
 QY 256 RIHLDMKVLFCVHLVSIPLSALNSSANPIIYFVGSRORONRNLKVLQALQDTP 315
 DB 241 RIHLDMKVLFCVHLVSIPLSALNSSANPIIYFVGSRORONRNLKVLQALQDTP 300
 QY 316 VDEGGWLPQETLTLGSRLEQ 337
 DB 301 VDEGGWLPQETLTLGSRLEQ 322
 RESULT 5
 MREGI_HUMAN STANDARD; PRT; 322 AA.
 AC 096LB2; Q8TDB8;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Mas-related G-protein coupled receptor member XI (Sensory neuron-
 specific G-protein coupled receptor 4).
 GN Name=MREGI; Synonyms=SNSR4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCBL_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2435808; PubMed=11551509;
 RA Dong X., Han S.-K., Zylika M.J., Simon M.I., Anderson D.J.;
 RT "A diverse family of GPCRs expressed in specific subsets of
 RT nociceptive sensory neurons."
 RL Cell 106:619-632(2001).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nrn15;
 RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
 RA Gosselin M., Fortin Y., Barville D., Shen S., Stroem P., Payza K.,
 RA Dray A., Walker P., Ahmad S.;
 RL "Proenkephalin A gene products activate a new family of sensory
 RL neuron-specific GPCRs."
 RL Nat. Neurosci. 5:201-209(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040266; PubMed=12044878;
 RA Takeda S., Kadowaki S., Haga T., Takasuo H., Mitaku S.;
 RT "Identification of G protein-coupled receptor genes from the human
 RT genome sequence."
 RL FEBS Lett. 520:97-101(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 CC nociceptive neurons. May regulate nociceptor function and/or
 CC development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins including BAM22 (bovine adrenal
 CC medulla peptide 22) and BAM (8-22). BAM22 is the most potent
 CC compound and evoked a large and dose-dependent release of
 CC intracellular calcium in stably transfected cells. G(alpha)q
 CC proteins are involved in the calcium-signaling pathway.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 CC root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Mas subfamily.
 CC
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DR EMBL, AF474989; AAL86881.1; -
 DR EMBL, AB083628; BAB89341.1; -
 DR EMBL, AB065846; BAC06064.1; -
 DR MIM; 607227; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein, Polymorphism, Transmembrane.
 FT DOMAIN 1 31
 FT TRANSMEM 32 52
 FT DOMAIN 53 67
 FT TRANSMEM 68 88
 FT DOMAIN 89 96
 FT TRANSMEM 97 117
 FT DOMAIN 118 144
 FT TRANSMEM 145 165
 FT DOMAIN 166 177
 FT TRANSMEM 178 198

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CC  DOMAIN 199 221 Cytoplasmic (Potential).
CC  TRANSMEM 222 242 6 (Potential).
CC  DOMAIN 243 254 Extracellular (Potential).
CC  TRANSMEM 255 275 7 (Potential).
CC  DOMAIN 276 322 Cytoplasmic (Potential).
CC  CARBOHYD 16 16 N-linked (GLCNAC...) (Potential).
CC  VARIANT 36 36 I -> V (in dbSNP:11024885).
CC  CONFLICT 5 5 /P1Id=VAR_019432.
CC  SEQUENCE 322 AA; 36250 MW; C7F3A9F4418B8AD1 CRC64;
Query Match 78.4%; Score 1383; DB 1; Length 322;
Best Local Similarity 83.5%; Pred. No. 2, 4e-93;
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELPINGREETPCYKOTLSFTGLTCTIVSLVATGNAVAVMLGCRMRNA 75
DB 1 MDPTISTLDTELPINGREETPCYKOTLSFTGLTCTIVSLVATGNAVAVMLGCRMRNA 60

QY 76 VSTIYIINLVADPLFLSGHICSPRLINIRHPIKSLISVMPFPYFGISMLSAISTER 135
DB 61 FSTIYIINLVADPLFLSGHICSPRLINIRHPIKSLISVMPFPYFGISMLSAISTER 120

QY 136 CSTIIPWYHCRPRYLSVWCVLWALSLRSILEMFCDFLFGSDSVWCETSDFIT 195
DB 121 CSTIIPWYHCRPRYLSVWCVLWALSLRSILEMFCDFLFGSDSVWCETSDFIT 180

QY 196 IANLVPLCVVLCSSVLVLRILCGSRKMPRLTYTILLTVLVFLCGPFGIQMALFS 255
DB 181 VAMLVPLCVVLCSSVLVLRILCGSRKMPRLTYTILLTVLVFLCGPFGIQMALFS 240

QY 256 RIHLDMKVLFCGHVLYSIFLSALNSSANPFIYFVGSFRORORONKLVQLQALDTPB 315
DB 241 RIHLDMKVLFCGHVLYSIFLSALNSSANPFIYFVGSFRORORONKLVQLQALDTPB 300

QY 316 VDEGGMLPOETLELSSGRLEQ 337
DB 301 VDEGGMLPOETLELSSGRLEQ 322

RESULT 6
SNES HUMAN STANDARD; PRT; 322 AA.
ID _GNS5_HUMAN
AC 08TDD7;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sensor neuron-specific G-protein coupled receptor 5.
GN Name=SNRS5;
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxId=9606;
OX [1]
RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/m815;
RX Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RX Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RX Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
RX Dray A., Walker P., Ahmad S.;
RA "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs."
RL Nat. Neurosci. 5:201-209(2002).
CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
CC nociceptive neurons. May regulate nociceptor function and/or
CC development, including the sensation or modulation of pain.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
CC root and trigeminal sensory neurons.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.

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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, AF474991; AAL86882.1; -
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCR_Rhodopsin.
CC PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 31 Extracellular (Potential).
CC TRANSMEM 32 52 1 (Potential).
CC DOMAIN 53 60 Cytoplasmic (Potential).
CC TRANSMEM 61 81 2 (Potential).
CC TRANSMEM 82 96 Extracellular (Potential).
CC TRANSMEM 97 117 3 (Potential).
CC DOMAIN 118 137 Cytoplasmic (Potential).
CC TRANSMEM 138 158 4 (Potential).
CC DOMAIN 159 177 Extracellular (Potential).
CC TRANSMEM 178 198 5 (Potential).
CC DOMAIN 199 218 Cytoplasmic (Potential).
CC TRANSMEM 219 239 6 (Potential).
CC DOMAIN 240 254 Extracellular (Potential).
CC TRANSMEM 255 275 7 (Potential).
CC DOMAIN 276 322 Cytoplasmic (Potential).
CC CARBOHYD 89 89 N-linked (GLCNAC...) (Potential).
CC SEQUENCE 322 AA; 36423 MW; 3D6FBA5DDFDD90 CRC64;
Query Match 78.4%; Score 1382; DB 1; Length 322;
Best Local Similarity 83.8%; Pred. No. 2, 9e-93;
Matches 269; Conservative 20; Mismatches 32; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELPINGREETPCYKOTLSFTGLTCTIVSLVATGNAVAVMLGCRMRNA 75
DB 1 MDPTISTLDTELPINGREETPCYKOTLSFTGLTCTIVSLVATGNAVAVMLGCRMRNA 60

QY 76 VSTIYIINLVADPLFLSGHICSPRLINIRHPIKSLISVMPFPYFGISMLSAISTER 135
DB 61 VSTIYIINLVADPLFLSGHICSPRLINIRHPIKSLISVMPFPYFGISMLSAISTER 120

QY 136 CSTIIPWYHCRPRYLSVWCVLWALSLRSILEMFCDFLFGSDSVWCETSDFIT 195
DB 121 CSTIIPWYHCRPRYLSVWCVLWALSLRSILEMFCDFLFGSDSVWCETSDFIT 180

QY 196 IANLVPLCVVLCSSVLVLRILCGSRKMPRLTYTILLTVLVFLCGPFGIQMALFS 255
DB 181 VAMLVPLCVVLCSSVLVLRILCGSRKMPRLTYTILLTVLVFLCGPFGIQMALFS 240

QY 256 RIHLDMKVLFCGHVLYSIFLSALNSSANPFIYFVGSFRORORONKLVQLQALDTPB 315
DB 241 RIHLDMKVLFCGHVLYSIFLSALNSSANPFIYFVGSFRORORONKLVQLQALDTPB 300

QY 316 VDEGGMLPOETLELSSGRLEQ 335
DB 301 VDEGGMLPOETLELSSGRLEQ 320

RESULT 7
MRG4 HUMAN STANDARD; PRT; 322 AA.
ID MRG4_HUMAN
AC 09ELN9; 08TDD6;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Mas-related G-protein coupled receptor member X4 (Sensory neuron-
DE specific G-protein coupled receptor 6).
GN Name=MRG4; Synonyms=SNRS6;
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21435808; PubMed=11551509;
 RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
 RT "A diverse family of GPCRs expressed in specific subsets of
 RT nociceptive sensory neurons."
 RL Cell 106:619-632(2001).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nrn815;
 RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labaree M.,
 RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Paya K.,
 RA Dray A., Walker P., Ahmad S.;
 RT "Proenkephalin A gene products activate a new family of sensory
 RT neuron-specific GPCRs."
 RL Nat. Neurosci. 5:201-209(2002).
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 CC nociceptive neurons. May regulate nociceptive function and/or
 CC development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 CC root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Mas subfamily.
 CC -----
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 CC -----
 CC EMBL; AY042216; AAK91807.1; -
 CC EMBL; AF474992; AAL86883.1; -
 CC MIM; 607230; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL 2; 1.
 KM G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
 FT DOMAIN 1 31
 FT TRANSMEM 32 52
 FT DOMAIN 53 60
 FT TRANSMEM 61 81
 FT DOMAIN 82 96
 FT TRANSMEM 97 117
 FT DOMAIN 118 137
 FT TRANSMEM 138 158
 FT DOMAIN 159 177
 FT TRANSMEM 178 198
 FT DOMAIN 199 218
 FT TRANSMEM 219 239
 FT DOMAIN 240 254
 FT TRANSMEM 255 275
 FT TRANSMEM 276 322
 FT CARBOHYD 25 25
 FT CARBOHYD 89 89
 FT VARIANT 8 8
 FT VARIANT 25 25
 FT VARIANT 54 54
 FT VARIANT 83 83
 FT CONFLICT 182 182

FT CONFLICT 319 319 R -> K (in Ref. 2).
 SQ SEQUENCE 322 AA; 36434 MW; 7CA676F8BD390A31 CRC64;
 Query Match 77.5%; Score 1367; DB 1; Length 322;
 Beef Local Similarity 83.1%; Pred. No. 3.6e-92;
 Matches 266; Conservative 20; Mismatches 34; Indels 0; Gaps 0;
 QY 16 MDSTIPVAGTELTPTINGREETPCYKQTLSPFTGLCTIVSLVATGNAAVVLTCGRMRNA 75
 DB 1 MDPTVPVGTGLTPTINGREETPCYNQTLSPFTGLCTIVSLVATGNAAVVLTCGRMRNA 60
 QY 76 VSIYILNVAADDFLSCSHITCSPLRLINRHPISKILSPMTPTPTGSMISAISTER 135
 DB 61 VSIYILNVAADDFLSCSHITCSPLRLINRHPISKILSPMTPTPTGSMISAISTER 120
 QY 136 CISTIPMPVHCRRPRYSYVCMVLTSLRSITLSEMPCDPFGSADSWCETSPFIT 195
 DB 121 CISTVMPVHCRRPRYSYVCMVLTSLRSITLSEMPCDPFGSADSWCETSPFIT 180
 QY 196 IAMLVFLCVLTCGSLVLLVRLTSGSRMPLRLVYVTLVFPVLLCGPFGIQLWALFS 255
 DB 191 VAMLIFFLCVVLCSGLVLLVRLTSGSRMPLRLVYVTLVFPVLLCGPFGIQLWALFS 240
 QY 256 RHLDMKVLFCGHVLSIFLSALNSANPITFFVGSFRQRONQNKVLRALQTPRE 315
 DB 241 RHMHLNLEVLCHVYLVCMSSLSLNSANPITFFVGSFRQRONQNKVLRALQTPRE 300
 QY 316 VDEGGWLPQRTLELSSGRL 335
 DB 301 VDKRGQLPRESLSSGRL 320
 RESULT 8
 MSG2_HUMAN
 ID MSG2_HUMAN STANDARD; PRT; 330 AA.
 AC Q96LB1;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Mas-related G-protein coupled receptor member X2.
 GN Name=MRG2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21435808; PubMed=11551509;
 RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
 RT "A diverse family of GPCRs expressed in specific subsets of
 RT nociceptive sensory neurons."
 RL Cell 106:619-632(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040266; PubMed=12044878;
 RA Takeda S., Kadowaki S., Haga T., Takasu H., Mitaku S.;
 RT "Identification of G protein-coupled receptor genes from the human
 RT genome sequence."
 RL FEBS Lett. 520:97-101(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tautsuni S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisen F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywiński M.I., Skalek U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (5)
RP TISSUE SPECIFICITY, AND POSSIBLE FUNCTION.
RX PubMed=12915402; DOI=10.1074/jbc.M302456200;
RA Robas N., Mead E., Fildock M.;
RT "MrgX2 is a high potency corticistatin receptor expressed in dorsal root
RT ganglion.";
RL J. Biol. Chem. 278:44400-44404(2003).
CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
CC nociceptive neurons. May regulate nociceptor function and/or
CC development, including the sensation or modulation of pain.
CC Corticistatin-14 seems to be a high potency ligand at this receptor.
CC Corticistatin has several biological functions including roles in
CC sleep regulation locomotor activity, and cortical function. In
CC intracellular-expressing cells, corticistatin-stimulated increases in
CC intracellular Ca(2+) but had no effect on basal or forskolin-
CC stimulated cAMP levels, suggesting that this receptor is G(q)-
CC coupled.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Has a limited expression profile, both
CC peripheral and within the central nervous system, with highest
CC levels in dorsal root ganglion.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AY042214; AAK91805.1; -;
DR EMBL, AB083626; BAB89339.1; -;
DR EMBL, AB065811; BAC06030.1; -;
DR EMBL, BC063450; AAH63450.1; -;
DR MIM: 607228; -;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tmr_1, 1.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Polymorphism; Transmembrane.
FT DOMAIN 1 33
FT TRANSMEM 34 54
FT TRANSMEM 55 63
FT TRANSMEM 64 84
FT TRANSMEM 85 96
FT TRANSMEM 97 117
FT TRANSMEM 118 144
FT TRANSMEM 145 165
FT TRANSMEM 166 184
FT TRANSMEM 185 205
FT TRANSMEM 206 228
FT TRANSMEM 229 249
FT DOMAIN 250 264
FT Extracellular (Potential).

FT TRANSMEM 265 285 7 (Potential).
FT DOMAIN 286 330 Cytoplasmic (Potential).
FT VARIANT 62 62 N->S (in dbSNP:10833049).
FT VARIAT 62 62 /FTID=VAR_019433.
SQ SEQUENCE 330 AA; 37099 MW; 0B328FD781DFEBE CRC64;
Query Match 56.1%; Score 989.5; DB 1; Length 330;
Best Local Similarity 62.1%; Pred. No. 1.5e-64;
Matches 208; Conservative 27; Mismatches 79; Indels 21; Gaps 5;
QY 16 MDSTIPVLTETLPINGREET---PCYKOTLSPTGTCVSLVALTGNVATMLCCRR 72
DB 1 MPPTTAMGTSTVTVGNQDALLLCKGKTLIPVFILFIALVGLGNGFVLLCFRRK 60
QY 73 RNNAVSYIINVAADPLFSGHI-----CSPLALINRHPISKLSPVMPFPYF 122
DB 61 RNAFSVYVLSLGAADPLFCQIINCLVYLSNFECS---ISINFP--SPFTVMCAVL 114
QY 123 IGLSMUASTRCLSLIPIWYHCRPRYLSVSMCVLLMALSLRSILEMPCDFLPSG 182
DB 115 AGLSMLSTWSTERCLSVLPWYRCRPRHLSAVCVLLMALSLSLISLEGKCGFLFD 174
QY 183 ADSVWCETSDPTITAMVFLCVLLCGSSLVLLVRLICGSRKMPRLVYTLITVLPFL 242
DB 175 GDSGWCQTFDPTIAAWLIFLPMVLGSSIALVRLICGSRGPLEFRLYTLITVLPFL 234
QY 243 CGIPFGIOWFLIMWKDSDVFCFHPVSVVLSINSANPIYFVGSFRKQMLQOP 301
DB 235 CGIPFGIOWFLIMWKDSDVFCFHPVSVVLSINSANPIYFVGSFRKQMLQOP 294
QY 302 -LKLVLORALOPTPEYDESGMPLQETLISGRL 335
DB 295 LKLVLORALOPTPEYDESGMPLQETLISGRL 329
RESULT 9
AAH63450 PRELIMINARY; PRT; 330 AA.
AC AAH63450; PRELIMINARY; PRT; 330 AA.
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor MRGX2.
CN MRGX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
OX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisen F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalek U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC063450; AAB63450.1; -
 KW Receptor.
 SQ SEQUENCE 330 AA; 37099 MW; 0B328FD78B1D66B CRC64;

Query Match 56.1%; Score 989.5; DB 2; Length 330;
 Best Local Similarity 62.1%; Pred. No. 1.5e-64;
 Matches 208; Conservative 27; Mismatches 79; Indels 21; Gaps 5;

QY 16 MDSTIPVLGTELPINGREET--PCYKQTLSTGLTCIVSLVALTGNAVIMLLGCMR 72
 DB 1 MDPTTPAMGTESTVINGNDQALLLCGKETLIPVFLIFALVGVANGFVLMILGFRR 60
 QY 73 RNVSITILNVADFLFLSHIT-----CSPLRLINIRPIKISLPWTFFYP 122
 DB 61 RNAPSVYVLSLAGDFLFCQIINCIVLYLSNPFCS---ISINPP-SFTTWTCAVL 114
 QY 123 IGLSMLSAISTERCLSIPIWYHCRPRYLSVNCVLLMALSLRSILEMMFCDFLPSG 182
 DB 115 AGLSMLSTVSTERCLSIPIWYHCRPRHLSAVCVLLMALSLSLILEGKFGFLSD 174
 QY 183 ADSVWCETSDPTITAMVFLCVLGGSSLVLLVRLICGSRKMPRLRYVITLLVLPFL 242
 DB 175 GDSGMCCTPDPITAMVFLFMVLCGSSLLVRLICGSRGLPLRLYVITLLVLPFL 234
 QY 243 CGLPFGIQLMFSRIHDMKVLFGVHLVSIFLSALNSANPIYFFVSGFRORONRON- 301
 DB 235 CGLPFGIQLMFSRIHDMKVDLFCIHVSVLSLSLNSANPIYFFVSGFRKQRLQOP 294
 QY 302 -LKVLVLRALODTPEVDEGGGMLPOETLELGSRL 335
 DB 295 ILKVLVLRALODIAEVDSHSCFRQGTPEMSRSL 329

RESULT 10
 Q7TN42 PRELIMINARY; PRT; 323 AA.
 ID Q7TN42
 AC Q7TN42
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MRGCG G protein-coupled receptor.
 GN Name=Mrgc;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=22810130; PubMed=12909716;
 RA Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
 RT "Atypical expansion in mice of the sensory neuron-specific Mrg G
 RT protein-coupled receptor family";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
 DR EMBL: AF518245; AA008317.1; -
 DR GO; GO:0016021; C:integral to membrane, IEA.
 DR GO; GO:0004872; P:receptor activity, IEA.
 DR GO; GO:0001884; F:rhodopsin-like receptor activity, IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalling, IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PROSITE: PS00237; G_PROTEIN_RECBP_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECBP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 323 AA; 37136 MW; 50639FDA42E8052 CRC64;

Query Match 46.7%; Score 823.5; DB 2; Length 323;
 Best Local Similarity 52.8%; Pred. No. 2.1e-52;
 Matches 172; Conservative 51; Mismatches 92; Indels 11; Gaps 6;

QY 16 MDSTIPVLGTELPINGREETPCYKQTLSTGLTCIVSLVALTGNAVIMLLGCMR 75
 DB 1 MDPTTPAMGTESTVINGNDQALLLCGKETLIPVFLIFALVGVANGFVLMILGFRR 59
 QY 76 VSIITILNVADFLFLSHITCSPLRLINIRPIKISLPWTFFYP 130
 DB 60 ISVYVLSLSDSFFLCCFIDSLMRIMNFGYVHLKSKRIIGNAVPIYISGLSLA 119
 QY 131 ISTERCLSIPIWYHCRPRYLSVNCVLLMALSLRSILEMMFCDFLPSGADVWCET 190
 DB 120 ISTERCLSVLPPIWYHCRPRHLSAVCVLLMALSLSLILEGKFGFLSD 178
 QY 191 SDPTITAMVFLCVLGGSSLVLLVRLICGSRKMPRLRYVITLLVLPFLCGLPFGIQ 250
 DB 179 VDFITVAVLFLFMVLCGSSLLVRLICGSRKMPRLRYVITLLVLPFLCGLPGLY 238
 QY 251 WAL--FSRIHDMKVLFGVHLVSIFLSALNSANPIYFFVSGFRORONRONKVLQR 308
 DB 239 LFLYVFGIHLAYP--FCHIVQVTVLLSCVSSANPIYFFVSGFRKRXRLKRVLKR 296
 QY 309 ALDPTPEVDEGGGMLPOETLELGSRL 334
 DB 297 ALDPTPEVDEYTDHSHVQKPTISERR 322

RESULT 11
 SNS1_RAT STANDARD; PRT; 323 AA.
 ID SNS1_RAT
 AC OBRAG1.
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sensory neuron-specific G-protein coupled receptor 1.
 GN Name=Snrt1; Synonyms=Snrt;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nr815;
 RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
 RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
 RA Dray A., Walker P., Ahmad S.;
 RT "Proenkephalin A gene products activate a new family of sensory
 RT neuron-specific GPCRs";
 RL Nat. Neurosci. 5:201-209(2002).
 CC -!- FUNCTION: Orphan receptor. Probably involved in the function of
 CC nociceptive neurons. May regulate nociceptor function and/or
 CC development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins (By similarity).
 CC -!- TISSUE SPECIFICITY: Integral membrane protein.
 CC -!- SUBCELLULAR LOCATION: Uniquely localized in a subset of small dorsal
 CC root and trigeminal sensory neurons. Associated preferentially
 CC with IB4 class of small-diameter somatosensory afferents (also
 CC known as nociceptors).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Maa subfamily.
 CC -----
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 CC -----
 DR EMBL: AF474986; AAL86877.2; ALT_INIT.
 DR RGD: 632284; Snrt1.
 DR InterPro: IPR000276; GPCR_Rhodpsn.

[illegible]

Proc. Natl. Acad. Sci. U.S.A. 99:14740-14745(2002).

[2]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Han S.-K., Dong X., Hwang J.-I., Zylka M.U., Anderson D.J.,

Simon M.I.;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY152435; C: integral to membrane; IEA.

DR GO: GO:0016021; C: integral to membrane; IEA.

DR GO: GO:0004872; F: receptor activity; IEA.

DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSIN.

DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SO SEQUENCE 322 AA; 36809 MW; 1E03CDD54AF89DC CRC64;

Query Match 45.2%; Score 797, DB 2; Length 322;

Best Local Similarity 53.2%; Pred. No. 1.8e-50;

Matches 174; Conservative 43; Mismatches 96; Indels 14; Gaps 8;

16 MDSITPVLGHELTPTINGREERPCCK-QTLSPTGLCTIVSLVALGNVAVLMLGCRMRN 74

1 MDPITSSHDVESTPTLNTGHPNCPIILTLT-LVLTITVLGAGNTIVMLLGFRRRK 58

75 AVSIYIINTLVADPLFLSGHITCSPLRLINL---RHPISK-IISPVTPEPYIGLSMTLS 129

59 AISTYIINTLVADPLFLSCFHIDSLNLTIDPYGLYARKLSGLDIGNAAIIPYISGLSILS 118

130 AISTERCISTIMPIWYHCRPRRYLSVWCYVLWALSLIRSTLEMMFCDFLPSGADSWCE 189

119 AISTERCICVLMPIWYHCHPRRNMSAIIICALIWLISFLMGILDW-FSGFLGETHHNLM-K 176

190 TSDITITAMLVFLCVLIGSSVLTVLVNLTIGSRKMPILTRLYVTLLTVLVFLGLPGGI 249

177 NVDTITITAPLFLFLMLLSSGLALLRLILCGPRKPSRLRYITVLTALVYVYLICGLPLGL 236

250 QWAL--FSRIHLDMKVLFCVHVLVSIPLASLNSANPIYFVYVSGFRQGRNMLKVLQ 307

237 YLFLIYFVGHVLP--FCHLYQVTVAVLSVNSANPIYIFLVSGFRQGRHRLSKVLK 294

308 PALQDTEPVEVGGWMLPQETLELSGR 334

295 RALQDTEPVEVGGWMLPQETLELSGR 321

RESULT 13

MGA_RAT

ID_MGA_RAT STANDARD; PRT; 304 AA.

AC 077N49;

DT 01-OCT-2004 (Rel. 45, Created)

DT 01-OCT-2004 (Rel. 45, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Maa-related G-protein coupled receptor member A.

GN Name=Mrgpra; Synonyms=Mrga;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

[1]

SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=22810130; PubMed=12909716; DOI=10.1073/pnas.1732949100;

RA Zylka M.U., Dong X., Southwell A.L., Anderson D.U.;

RT "Atypical expansion in mice of the sensory neuron-specific Mrg G

protein-coupled receptor family";

Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).

CC -1- FUNCTION: Orphan receptor. May regulate nociceptor function and/or

development, including the sensation or modulation of pain.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Mas subfamily.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF518238; AA008310.1; --
 DR KGD; 738050; Mrgpra.
 DR Interpro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 17
 FT 18 38
 FT 39 46
 FT 47 67
 FT 68 80
 FT 81 101
 FT 102 132
 FT 133 153
 FT 154 167
 FT 168 188
 FT 189 211
 FT 212 232
 FT 233 244
 FT 245 265
 FT 266 304
 FT 304 AA; 34334 MW; 4A820A4B0192E8B6 CRC64;
 SQ SEQUENCE

Query Match 44.4%; Score 782; DB 1; Length 304;
 Best Local Similarity 53.3%; Pred. No. 2,1e-49;
 Matches 176; Conservative 34; Mismatches 84; Indels 36; Gaps 8;

QY 16 MDSTIPVLGTELTPINGREPTCYKQTLSTFTGLCTIYS-LVALTGNAAVLTMLGCRMRN 74
 DB 1 MDKTIPT-----GSFNRKTLTP-----NLIIITIGVGLTGNAAVFWMLGFRLLARN 45
 QY 75 AVSIYIINLVAADEFLPSGHIIICSPRLINIRHP---ISKILSPWTPPYFGLSMLSAI 131
 DB 46 AFSVYIINLVAADEFLPSGHIIICSPRLINIRHP---ISKILSPWTPPYFGLSMLSAI 105
 QY 132 STERCISILMPWYHCRPRKPRYLSSVVCVLTMLALSLRSLIEMPCDFLFGADSVW---- 187
 DB 106 STERCISVVCPIWYRCRPRKPRYLSSVVCVLTMLALSLRSLIEMPCDFLFGADSVW---- 161
 QY 188 -CETSDPTITAMVFLCVLTCGSSLVLTALVRLICSGRKMPLTRLYVTILTVLVFLCGLP 246
 DB 162 RCLASNFPTAACLFPLFVVLCTLSIALLVRSFCGAGRKRLRLVATIMLVFLCGLP 221
 QY 247 FGIQWALFSRIHLDKVLFCFVHLVSIPLSALNSANDIYFFVGSFRORONRQNLKVL 306
 DB 222 FGIHMFLLIWKIDYGRKAYGLYLAALVLTAVNSCANPIYFFVGSFR-HQKHQTLKVL 280
 QY 307 QRALQDTPPEVDEGGWLPQETLELSGRLE 336
 DB 281 QRALQDTPETA-----NTVEMSSSKVE 303
 RESULT 14
 QY 091YB7 PRELIMINARY; PRT; 331 AA.
 AC 091YB7;
 DT 01-DEC-2001 (Tremblrel. 19; Created)
 DT 01-DEC-2001 (Tremblrel. 19; Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26; Last annotation update)
 DE G-protein coupled receptor.
 GN Name=rc 56.1.3;

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;

RP SEQUENCE FROM N.A.
 RX MEDLINE=22080228; PubMed=12084918;
 RA Bender E., Bust A., Jurzak M., Langlois X., Baggerman G.,
 RA Verhaesselt P., Ercken M., Guo H.Q., Wintemolders C.,
 RA Van den Wyngaert I., Van Oers I., Schoofs L., Luyten W.;
 RT "Characterization of an orphan G protein-coupled receptor localized in
 RT the dorsal root ganglia reveals adenine as a signaling molecule";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:8573-8578(2002).
 DR EMBL; AJ311952; CAC84592.1; --
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
 DR Interpro; IPR00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 331 AA; 37005 MW; 74BA8A8C557859AC CRC64;

Query Match 44.1%; Score 778; DB 2; Length 331;
 Best Local Similarity 53.3%; Pred. No. 4,5e-49;
 Matches 176; Conservative 33; Mismatches 85; Indels 36; Gaps 8;

QY 16 MDSTIPVLGTELTPINGREPTCYKQTLSTFTGLCTIYS-LVALTGNAAVLTMLGCRMRN 74
 DB 28 MDKTIPT-----GSFNRKTLTP-----NLIIITIGVGLTGNAAVFWMLGFRLLARN 72
 QY 75 AVSIYIINLVAADEFLPSGHIIICSPRLINIRHP---ISKILSPWTPPYFGLSMLSAI 131
 DB 73 AFSVYIINLVAADEFLPSGHIIICSPRLINIRHP---ISKILSPWTPPYFGLSMLSAI 132
 QY 132 STERCISILMPWYHCRPRKPRYLSSVVCVLTMLALSLRSLIEMPCDFLFGADSVW---- 187
 DB 133 STERCISVVCPIWYRCRPRKPRYLSSVVCVLTMLALSLRSLIEMPCDFLFGADSVW---- 188
 QY 188 -CETSDPTITAMVFLCVLTCGSSLVLTALVRLICSGRKMPLTRLYVTILTVLVFLCGLP 246
 DB 169 RCLASNFPTAACLFPLFVVLCTLSIALLVRSFCGAGRKRLRLVATIMLVFLCGLP 248
 QY 247 FGIQWALFSRIHLDKVLFCFVHLVSIPLSALNSANDIYFFVGSFRORONRQNLKVL 306
 DB 249 FGIHMFLLIWKIDYGRKAYGLYLAALVLTAVNSCANPIYFFVGSFR-HQKHQTLKVL 307
 QY 307 QRALQDTPPEVDEGGWLPQETLELSGRLE 336
 DB 308 QRALQDTPETA-----NTVEMSSSKVE 330
 RESULT 15
 QY 08CDY4 PRELIMINARY; PRT; 338 AA.
 AC 08CDY4;
 DT 01-MAR-2003 (Tremblrel. 23; Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23; Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26; Last annotation update)
 DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
 DE library, clone:4833406i20 product:MrgB2 G protein-coupled receptor,
 DE full insert sequence.
 GN Name=4833406i20Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 Kurihara C., Matsuyama T., Miyazaki R., Miyata M., Nakamura M.,
 Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK029369; BAC26422.1;
 RX MGI:2441674; 483406120Rik.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_P1_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECP_P1_2; 1.
 KW Receptor.
 SQ SEQUENCE 338 AA; 38866 MW; 7809FF787CEFC66 CRC64;

Matches 159; Conservative 48; Mismatches 99; Indels 12; Gaps 5;
 QY 13 PLMSDSTIVVLGHELPINGR---ERTPCYKQTLSTGLTCVSYALTCNNAVWLLGC 69
 DB || :
 5 FLKNLSTSAWKNTITVLNGSYFFDTSVCVTRQAMILLSTISLVGKGLNAVLFGLI 64
 QY 70 RRRNNAVSIIINLVADPLFL-SGHIIICSPRL-----INIRHPISKILSPVMTPEPYFI 123
 DB || :
 65 RHTNNAFTYIINLVADPLFLCSQFVLCILAFIYFSDINIP--VLYVPIRAYLS 122
 QY 124 GLSMLSAISTERCLSLMPDIWYHCRPRRYLSSVWCVLWALSRLSILEMFCDFLPSGA 183
 DB || :
 123 GSTIISTISIERCLSVIWPWYRCRPRHTSAITCFVLMWMSLLGLSGKAGGLFNSF 182
 QY 184 DSVWCETSPFITAMVFLCVLCSGLVLLVRIILCSKRMPLTRVYTLVTVVYELLC 243
 DB || :
 183 DSVWCETSPFITAMVFLCVLCSGLVLLVRIILCSKRMPLTRVYTLVTVVYELLC 242
 QY 244 GLPFGIOWALFSRIHDMKVLFCVHLVSIPLSALNSSANPIYFPVGSFRORQ-NRONTL 302
 DB || :
 243 GLPFGIOWALFSRIHDMKVLFCVHLVSIPLSALNSSANPIYFPVGSFRORQ-NRONTL 302
 QY 303 KLVLPALQDTPREVDECG 320
 DB || :
 303 KLVLPALQDTPREVDECG 320

Search completed: October 27, 2004, 08:33:33
 Job time : 192 secs

Query Match 43.3%; Score 763; DB 2; Length 338;
 Best Local Similarity 50.0%; Pred. No. 5.8e-48;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2004, 08:34:24 ; Search time 155 Seconds
(without alignments)
779.947 Million cell updates/sec

Title: US-09-867-570-2

Sequence: 1 MESKSWVIRLGLFSLMDSTI.....EGGWLPEFLRLSGRLAQ 337

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337	100.0	337	5	AAU97598 Human G-P
2	322	95.5	322	3	AAV90761 Human G P
3	322	95.5	322	5	ABU04077 Human G P
4	322	95.5	322	5	AAE21296 Human Mrg
5	322	95.5	322	5	AD116993 Human NOV
6	322	95.5	322	5	AD116998 Human NOV
7	322	95.5	322	6	ABP81750 Human G P
8	322	95.5	322	8	ADH08535 MrGX3_3/
9	322	95.5	322	8	AD044602 Human HIT
10	322	95.5	322	8	AD029705 Human GPC
11	322	95.5	560	7	ADP70481 Orphan re
12	277	82.2	322	8	ADF29105 Human GPC
13	224	66.5	322	3	AAAB14846 Human nov
14	221	65.6	322	3	AAV90762 Human G P
15	221	65.6	322	5	AD116994 Human NOV
16	221	65.6	322	5	AD116999 Human NOV
17	221	65.6	322	7	AD044604 Human GPC
18	221	65.6	322	8	AD044604 Human HIT
19	181	53.7	302	6	ABP96695 Human G P
20	166	49.3	304	2	AD12766 Human GPC
21	149	44.2	322	2	AAV30159 Human dor
22	100	29.7	318	7	AD12724 Human hum
23	89	26.4	440	4	ABG21073 Novel hum
24	86	25.5	322	2	AAV30160 Human dor
25	76	22.6	76	7	ADD18095 Human G-P

26	76	22.6	328	7	ADD18024 Human G-P
27	50	14.8	319	5	AD116638 Human NOV
28	50	14.8	319	8	ADN42292 Human nov
29	50	14.8	322	2	AAV30162 Human dor
30	50	14.8	322	4	AA644294 Human GTP
31	50	14.8	322	4	AAE12794 Human G P
32	50	14.8	322	5	AAU04371 Human G-P
33	50	14.8	322	5	AAE17074 Human G-P
34	50	14.8	322	5	ABP95617 Human GPC
35	50	14.8	322	5	AAE21288 Human MrG
36	50	14.8	322	5	AD116991 Human NOV
37	50	14.8	322	5	AD116636 Human NOV
38	50	14.8	322	5	AD116997 Human NOV
39	50	14.8	322	6	ABP96696 Human G P
40	50	14.8	322	6	ABP59266 Human Dor
41	50	14.8	322	7	AD086445 Human GPC
42	50	14.8	322	7	ABW00803 Human GPC
43	50	14.8	322	7	AD196466 Human G P
44	50	14.8	322	8	ADH08520 MrGX1_3/
45	50	14.8	322	8	ADN42290 Human nov

ALIGNMENTS

RESULT 1	
AAU97598	AAU97598 standard; protein; 337 AA.
AC	AAU97598;
XX	12-AUG-2002 (first entry)
DT	
XX	
DE	Human G-protein coupled receptor (GPCR).
XX	
KW	Human, G-protein coupled; receptor; GPCR; human protease;
KW	human therapeutic protein; query sequence; search; chromosome 3;
KW	sequence database; non-human transgenic animal; gene therapy.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Domain
FT	/label= Helix_1
FT	75..95
FT	/label= Helix_2
FT	112..132
FT	/label= Helix_3
FT	133..135
FT	/note="Protein kinase C (PKC) phosphorylation site"
FT	151..171
FT	/label= Helix_4
FT	169..172
FT	/note="Casein kinase II (CK2) phosphorylation site"
FT	181..184
FT	/note="Casein kinase II (CK2) phosphorylation site"
FT	193..213
FT	/label= Helix_5
FT	221..223
FT	/note="Protein kinase C (PKC) phosphorylation site"
FT	229..249
FT	/label= Helix_6
FT	244..249
FT	/note="Myristoylation site"
FT	248..253
FT	/note="Myristoylation site"
FT	261..281
FT	/label= Helix_7
FT	279..282
FT	/note="Ser phosphorylation site"
FT	292..294
FT	/note="Protein kinase C (PKC) phosphorylation site"
FT	333..336

PT /note= "Casein kinase II (CK2) phosphorylation site"
XX MO200234914-A1.
XX 02-MAY-2002.
XX 10-OCT-2001; 2001WO-US031592.
XX 25-OCT-2000; 2000US-00695045.
XX 31-MAY-2001; 2001US-00867570.
XX (BEKE) BE CORP NY.
XX
XX Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM,
XX
XX WPI; 2002-463360/49.
XX N-PSDB; ABK52822, ABK52823.
XX
XX Novel isolated G-protein coupled receptor peptide useful for treating
XX disorder characterized by absence of, in appropriate or unwanted
XX expression of the receptor protein, and as immunogens to raise
XX antibodies.
XX
XX Claim 1; Fig 2; 75pp; English.
XX
XX The present invention relates to a new G-protein coupled receptor (GPCR)
XX peptide. The invention is useful for identifying a modulator of GPCR and
XX for treating a disease or condition mediated by a human protease. The
XX invention is also useful as models for the development of human
XX therapeutics, for identifying therapeutic proteins, as targets for
XX development of human therapeutic agents, and as query sequence to perform
XX a search against sequence databases to, for e.g., identify other family
XX members of related sequences. The vector of the invention is useful for
XX producing a GPCR protein or peptide, for conducting cell-based assays
XX involving the GPCR protein or its fragment, for identifying GPCR protein
XX mutants whose functions are affected, and to produce non-human transgenic
XX animals. The present amino acid sequence represents the human G-protein
XX coupled receptor (GPCR) protein of the invention. This sequence is
XX encoded by the human G-protein coupled receptor (GPCR) gene located on
XX chromosome 3
XX
XX Sequence 337 AA;
SQ
Query Match 100.0%; Score 337; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESKSSWVIRLGFSLMDSTIPVLTGELTPINGREBTPCKQTLSFTGLCTIVSLVATGN 60
DB 1 MESKSSWVIRLGFSLMDSTIPVLTGELTPINGREBTPCKQTLSFTGLCTIVSLVATGN 60
QY 61 AVVAMLGCRMRNRNAVSIYILNVAADFLFSGHIICSPRLINIRHPISTKILSPWTFP 120
DB 61 AVVAMLGCRMRNRNAVSIYILNVAADFLFSGHIICSPRLINIRHPISTKILSPWTFP 120
QY 121 YFGLSMLSAISTERCLSIWPVWYHCRPRYLSVWCYLWALSILRSILEMFCDFLF 180
DB 121 YFGLSMLSAISTERCLSIWPVWYHCRPRYLSVWCYLWALSILRSILEMFCDFLF 180
QY 181 SGADSWCETSDFTITAVLFLCVLFCGSSLVLAIRILGSRKMPILTRYITILLTVLVF 240
DB 181 SGADSWCETSDFTITAVLFLCVLFCGSSLVLAIRILGSRKMPILTRYITILLTVLVF 240
QY 241 LLGGLPFGIOALFRIHLDKLVLCFCHVHLVSIIFLSALNSSANPIIYFVGSFRORONQ 300
DB 241 LLGGLPFGIOALFRIHLDKLVLCFCHVHLVSIIFLSALNSSANPIIYFVGSFRORONQ 300
QY 301 NLKVLQRLADTPEVDEGGGWLPOETLELSSRLQ 337
DB 301 NLKVLQRLADTPEVDEGGGWLPOETLELSSRLQ 337
RESULT 2

AA90761
ID AA90761 standard; protein, 322 AA.
XX
XX AC AA90761;
XX
XX DT 18-AUG-2000 (first entry)
XX
XX DE Human G protein-coupled receptor hH17T213 SEQ ID NO:1.
XX
XX KW Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
XX genetic disease; cellular function regulation.
XX
XX OS Homo sapiens.
XX
XX PN WO200020455-A1.
XX
XX PD 13-APR-2000.
XX
XX PF 30-SEP-1999; 99WO-JP005366.
XX
XX PR 01-OCT-1998; 98JP-00279535.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX PA Watanabe T, Terao Y, Matsui H;
XX
XX PI WPI; 2000-303747/26.
XX
XX DR N-PSDB; AAA29811.
XX
XX PT Human-derived G protein-coupled protein and encoding nucleic acid, useful
XX e.g. in determining ligands and treatment of diseases associated with
XX dysfunction of the protein.
XX
XX Claim 1; Page 90-91; 97pp; Japanese.
XX
XX The present sequence represents a human-derived G protein-coupled protein
XX designated hH17T213, which is isolated from the human hippocampus. The G
XX protein-coupled receptor can be used for preventing, treating and
XX diagnosing genetic diseases associated with G protein-coupled protein,
XX and for regulating cellular functions. The protein can be used to prevent
XX and treat disorders associated with G protein-coupled protein gene
XX dysfunction. It can also be used to identify G protein-coupled protein
XX ligands and generating antibodies and antisera against the protein. It is
XX also useful in constructing recombinant receptor protein expression
XX systems, developing receptor-binding assay systems and screening drug
XX candidates, and can be used as a probe in the genetic diagnosis of G
XX protein-coupled protein disorders
XX
XX Sequence 322 AA;
SQ
Query Match 95.5%; Score 322; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 2,9e-309;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MDSTIPVLTGELTPINGREBTPCKQTLSFTGLCTIVSLVATGNNAVVLGCRMRNRNA 75
DB 1 MDSTIPVLTGELTPINGREBTPCKQTLSFTGLCTIVSLVATGNNAVVLGCRMRNRNA 60
QY 76 VSIYILNVAADFLFSGHIICSPRLINIRHPISTKILSPWTFPFTIGSMLSAISTER 135
DB 76 VSIYILNVAADFLFSGHIICSPRLINIRHPISTKILSPWTFPFTIGSMLSAISTER 120
QY 136 CLSILMPVWYHCRPRYLSVWCYLWALSILRSILEMFCDFLFGADSWCETSDFT 195
DB 136 CLSILMPVWYHCRPRYLSVWCYLWALSILRSILEMFCDFLFGADSWCETSDFT 180
QY 196 IAVLFLCVLFCGSSLVLAIRILGSRKMPILTRYITILLTVLVFLCGPFGIOALFS 255
DB 196 IAVLFLCVLFCGSSLVLAIRILGSRKMPILTRYITILLTVLVFLCGPFGIOALFS 240
QY 256 RIHLDKLVLCFCHVHLVSIIFLSALNSSANPIIYFVGSFRORONQNLKVLQRLADTPE 315
DB 256 RIHLDKLVLCFCHVHLVSIIFLSALNSSANPIIYFVGSFRORONQNLKVLQRLADTPE 300

QY 316 VDEGGMLPQETLELSGSRLEQ 337
DB 301 VDEGGMLPQETLELSGSRLEQ 322

RESULT 3
ABJ04077
ID ABJ04077 standard; protein; 322 AA.
AC ABJ04077;
DT 11-OCT-2002 (first entry)
DE Human G protein coupled receptor hrUP37.
XX
XX
XX Human; G-protein coupled receptor; GPCR; hrUP28; hrUP29; hrUP30; hrUP31;
KM hrUP32; hrUP33; hrUP34; hrUP35; hrUP36; hrUP37.
XX
XX Homo sapiens.
OS
XX MO200242461-A2.
PN
XX 30-MAY-2002.
PD
XX 26-NOV-2001; 2001MO-US044386.
PF
XX 27-NOV-2000; 2000US-0253404P.
PR 12-DEC-2000; 2000US-025346P.
PR 20-FEB-2001; 2001US-0270266P.
PR 20-FEB-2001; 2001US-0270286P.
PR 06-APR-2001; 2001US-0282032P.
PR 06-APR-2001; 2001US-0282358P.
PR 06-APR-2001; 2001US-0282365P.
PR 14-MAY-2001; 2001US-0290917P.
PR 31-JUL-2001; 2001US-0309208P.
XX
XX (AREN-) ARENA PHARM INC.
PA
XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
PI
XX MPI; 2002-566565/60.
DR N-PSDB; ABT04875.
XX
XX Novel endogenous and non-endogenous versions of G protein-coupled
PT receptor useful for identification of candidate compounds as receptor
XX agonists or antagonists for use as therapeutic agents.
XX
XX Claim 37, Page 75-76; 84pp; English.
PS
XX The present invention provides the protein and coding sequences of
CC several human G-protein coupled receptors (GPCRs). These can be used in
CC the identification of candidate compounds as receptor agonists or inverse
CC agonists having applicability as therapeutic agents. The present sequence
CC is a GPCR protein of the invention
XX
XX Sequence 322 AA:

Query Match 95.5%; Score 322; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.9e-309;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIVLGTETLPINGRETPCYKOTLSFTGTCIVSLVATLGNNAVVTMLGCRMRNA 75
DB 1 MDSTIVLGTETLPINGRETPCYKOTLSFTGTCIVSLVATLGNNAVVTMLGCRMRNA 60
QY 76 VSIYIINLVADPLFSGHITCSPIRLINIRHPISTKLSVMTFPYRIGLSMISAISTER 135
DB 61 VSIYIINLVADPLFSGHITCSPIRLINIRHPISTKLSVMTFPYRIGLSMISAISTER 120
QY 136 CUSILPIWYHCRPRYLSVMCVLLMALSLRSILEMFCDFLFGSADSVWCETSDPIT 195

DB 121 CUSILPIWYHCRPRYLSVMCVLLMALSLRSILEMFCDFLFGSADSVWCETSDPIT 180
QY 196 IAMLVFLCVLLCGSSLVLRILCGSRKMPRLRYTTLTTLVFLCGLPFGIOWALFS 255
DB 181 IAMLVFLCVLLCGSSLVLRILCGSRKMPRLRYTTLTTLVFLCGLPFGIOWALFS 240
QY 256 RIHLDMKVLFCVHVLVSIPLSALNSANPIIYFVGSFRORONRQNLQBALQDTPR 315
DB 241 RIHLDMKVLFCVHVLVSIPLSALNSANPIIYFVGSFRORONRQNLQBALQDTPR 300
QY 316 VDEGGMLPQETLELSGSRLEQ 337
DB 301 VDEGGMLPQETLELSGSRLEQ 322

RESULT 4
AAE21296
ID AAE21296 standard; protein; 322 AA.
XX
XX AAE21296;
AC
XX
XX 01-JUL-2002 (first entry)
DT
XX
XX Human MrgX3 (mas-related gene) protein.
DE
XX
XX Human; mas-related gene; G-protein coupled receptor; drg-12 protein;
KM receptor; sensory perception; pain; analgesic; MrgX3.
XX
XX Homo sapiens.
OS
XX MO200183555-A2.
PN
XX 08-NOV-2001.
PD
XX 04-MAY-2001; 2001MO-US014519.
PF
XX 04-MAY-2000; 2000US-0202027P.
PR 01-AUG-2000; 2000US-0222344P.
PR 03-NOV-2000; 2000US-00704707.
PR 19-APR-2001; 2001US-0285493P.
XX
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
PA
XX Anderson DJ, Dong X, Zylka M, Han S, Simon M;
PI
XX MPI; 2002-171346/22.
DR N-PSDB; AAD33751.
XX
XX Isolated polypeptide, Mrg, which is a G-protein coupled receptor and an
PT isolated polypeptide, drg-12, which is also a receptor, useful for
XX identifying agonists or antagonists for treating pain.
XX
XX Claim 16; Page 130; 185pp; English.
PS
XX The invention relates to Mrg (mas-related gene) protein, which is a G-
CC protein coupled receptor and drg-12 protein, which is a receptor. The
CC invention is useful for identifying compounds that bind to it, especially
CC agonists or antagonists. Administration of an agent (e.g. the identified
CC agonist) that increases the expression of Mrg in a mammal may be used for
CC treating impaired sensory perception in a mammal, especially pain. The
CC antagonist may also be useful for treating impaired sensory perception in
CC a mammal. The present sequence is human MrgX3 protein
XX
XX Sequence 322 AA:

Query Match 95.5%; Score 322; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.9e-309;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIVLGTETLPINGRETPCYKOTLSFTGTCIVSLVATLGNNAVVTMLGCRMRNA 75
DB 1 MDSTIVLGTETLPINGRETPCYKOTLSFTGTCIVSLVATLGNNAVVTMLGCRMRNA 60

QY 76 VSIYILNVAADFLFLSGHIICSPRLINIRHPISKILSPVTPFYFGLSMLSAISTER 135
 DB 61 VSIYILNVAADFLFLSGHIICSPRLINIRHPISKILSPVTPFYFGLSMLSAISTER 120
 QY 136 CLSTLMPWYHCRPRVYSSWCVLLMLSLRSLLEWPCDFLPSGADSVWCERSDFT 195
 DB 121 CLSTLMPWYHCRPRVYSSWCVLLMLSLRSLLEWPCDFLPSGADSVWCERSDFT 180
 QY 196 IAWLVLFCVVGCGSSLVLVLRILCGSRKMPLTRLYVTILLFVLVFLCGLPFGIOMALFS 255
 DB 181 IAWLVLFCVVGCGSSLVLVLRILCGSRKMPLTRLYVTILLFVLVFLCGLPFGIOMALFS 240
 QY 256 RIHLDMKVLFCGHVLSIFLSALNSSANPIYFVGSFRORONKLVLORALQDTP 315
 DB 241 RIHLDMKVLFCGHVLSIFLSALNSSANPIYFVGSFRORONKLVLORALQDTP 300
 QY 316 VDEGGWLPORTELSSGRLQ 337
 DB 301 VDEGGWLPORTELSSGRLQ 322

RESULT 5

AD116993
 ID AD116993 standard; protein, 322 AA.

AC AD116993;

DT 15-APR-2004 (first entry)

DE Human NOVA protein homologue SegID 529.

KW human; NOVA; cardiomyopathy; atherosclerosis; cancer; diabetes;

KW inflammation; autoimmune disorder; allergy; blood disorder;

KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;

KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;

KW Alzheimer's disease; infection; etc.

OS Homo sapiens.

PN MO200268649-A2.

PD 06-SEP-2002.

PF 31-JAN-2002; 2002WO-US002785.

PR 31-JAN-2001; 2001US-0265395P.

PR 31-JAN-2001; 2001US-0265412P.

PR 31-JAN-2001; 2001US-0265514P.

PR 02-FEB-2001; 2001US-0266406P.

PR 05-FEB-2001; 2001US-0266767P.

PR 07-FEB-2001; 2001US-0266957P.

PR 08-FEB-2001; 2001US-0267057P.

PR 09-FEB-2001; 2001US-0267823P.

PR 15-FEB-2001; 2001US-0268974P.

PR 26-FEB-2001; 2001US-0271664P.

PR 27-FEB-2001; 2001US-0271839P.

PR 02-MAR-2001; 2001US-0272788P.

PR 02-MAR-2001; 2001US-0273046P.

PR 14-MAR-2001; 2001US-0275925P.

PR 14-MAR-2001; 2001US-0275950P.

PR 14-MAR-2001; 2001US-0275989P.

PR 15-MAR-2001; 2001US-0276448P.

PR 15-MAR-2001; 2001US-0276450P.

PR 16-MAR-2001; 2001US-0276397P.

PR 16-MAR-2001; 2001US-0276768P.

PR 20-MAR-2001; 2001US-0278652P.

PR 26-MAR-2001; 2001US-0278775P.

PR 29-MAR-2001; 2001US-0279882P.

PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282929P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.

Tchernev VT, Spytek KA, Zernušen BD, Patturajan M, Shinkets RA,

Li U, Gangoli EA, Padigaru M, Anderson DM, Rastelli L, Miller CB,

Gerlach VL, Taupier R, Gusev VY, Colman SD, Wolenc AR, Pena CE,

Furtak K, Grose WM, Albrook JP, Lepley DM, Rieger DK, Burgess CB,

WPI: 2002-706998/76.

PT New NOVA polypeptides and nucleic acids, useful for preventing or

PT treating NOVA-associated disorders, e.g. cancer, cardiomyopathy,

PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX This invention relates to a novel nucleic acids, and encoded polypeptides

XX thereof, which have properties related to the stimulation of biochemical

XX or physiological responses in a cell, tissue, organ or organism.

XX Specifically, it refers to the use of biologically active fragments for

XX diagnostic and prognostic assays and furthermore in the treatment of

XX human and murine NOVA proteins, as well as methods to modulate their

XX expression using antisense oligos, ribozymes and peptide nucleic acids.

XX The NOVA polypeptides, polynucleotides and antibodies are useful in

XX treating or preventing NOVA-associated disorders, e.g. cardiomyopathy,

XX atherosclerosis, cancer and diabetes. Furthermore, they may be used in

XX treating or preventing diseases such as inflammation, autoimmune

XX disorders, allergies, blood disorders, acquired immunodeficiency syndrome

XX (AIDS), obesity, aschma, immunoglobulin (Ig)A nephropathy, cirrhosis,

XX arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy

XX and epilepsy. Accordingly, these molecules have many activities including

XX cytoskeletal, cardiac, anti-inflammatory, immunosuppressive, antiallergic,

XX haemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,

XX antiaesthetic, nephroprotective, antibacterial, hepatotropic,

XX neuroprotective, nootropic, antiviral, antiparasitic,

XX relaxant and anticonvulsant. In addition, they are useful in screening

XX assays to identify small molecules that modulate or inhibit, for example,

XX neurogenesis, wound healing and angiogenesis. The nucleic acids are also

XX used as in chromosome mapping, tissue typing, preventive medicine and

XX pharmacogenomics. This polypeptide is a homologue of a human NOVA protein

XX of the invention.

XX Sequence 322 AA;

Query Match

95.5%; Score 322; DB 5; Length 322;

Best Local Similarity 100.0%; Pred. No. 2.9e-309;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVGLPRLPINKRETPCKQKLTSTGLTCLVSLVAGNNAVMLLGRMRNA 75
DB 1 MDSTIPVGLPRLPINKRETPCKQKLTSTGLTCLVSLVAGNNAVMLLGRMRNA 60
QY 76 VSIYIINLVADPLFLSGHIIICSPRLINIRHPIKSLSPVMTPEYPIGSMLSAISTER 135
DB 61 VSIYIINLVADPLFLSGHIIICSPRLINIRHPIKSLSPVMTPEYPIGSMLSAISTER 120
QY 136 CLSLIPWYHCRPRPRLTSSVWCYLLWALSILRSIEMFCDFLPSGADSVWCETSDFIT 195
DB 121 CLSLIPWYHCRPRPRLTSSVWCYLLWALSILRSIEMFCDFLPSGADSVWCETSDFIT 180
QY 196 IAWLVPLCVLCCSSLVLLVRIICGSRKMP/LRLYXTIITLVVFLICGPFQIOWALFS 255
DB 181 IAWLVPLCVLCCSSLVLLVRIICGSRKMP/LRLYXTIITLVVFLICGPFQIOWALFS 240
QY 256 RIHLDMVLFCHVHLVSIPLSALNSSANPITTYFVGSFRORONRKL/LORALODTPE 315
DB 241 RIHLDMVLFCHVHLVSIPLSALNSSANPITTYFVGSFRORONRKL/LORALODTPE 300
QY 316 VDEGGGWLPOETLELSSGRLEQ 337
DB 301 VDEGGGWLPOETLELSSGRLEQ 322

RESULT 6
AD116998
ID AD116998 standard; protein; 322 AA.
AC AD116998;
XX
DT 15-APR-2004 (first entry)
XX
DE Human NOVX protein homologue Segid 534.
XX
KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune-disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.
XX
OS Homo sapiens.
XX
PN WO200268649-A2.
XX
PD 06-SEP-2002.
XX
PF 31-JAN-2002; 2002MO-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.

PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279682P.
PR 29-MAR-2001; 2001US-0279684P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.
XX
PA Tchernev VT, Spytek KA, Zernhusen BD, Patuvarajan M, Shinkets RA;
XX Li L, Gangolli EA, Padigan M, Anderson DW, Raetelli L, Miller CE;
XX Gerlach VL, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CE;
XX Pirtak K, Grosse WM, Alsbrook UP, Lepley DM, Rieger DK, Burgess CE;
XX WPI; 2002-706998/76.
XX
DR New NOVX polypeptides and nucleic acids, useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
XX pharmacogenomics.
XX
PS Disclosure; SEQ ID NO 534; 1498bp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
XX thereof, which have properties related to the stimulation of biochemical
XX or physiological responses in a cell, tissue, organ or organism.
XX Specifically, it refers to the use of biologically active fragments for
XX diagnostic and prognostic assays and furthermore in the treatment of
XX diverse pathological conditions. The present invention describes novel
XX human and murine NOVX proteins, as well as methods to modulate their
XX expression using antisense oligos, ribozymes and peptide nucleic acids.
XX The NOVX polypeptides, polynucleotides and antibodies are useful in
XX treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
XX atherosclerosis, cancer and diabetes. Furthermore, they may be used in
XX treating or preventing diseases such as inflammation, autoimmune
XX disorders, allergies, blood disorders, acquired immunodeficiency syndrome
XX (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
XX arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
XX and epilepsy. Accordingly, these molecules have many activities including
XX cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
XX hemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
XX antistimatic, nephrotropic, antiarthritic, hepatotropic,
XX neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
XX relaxant and anticonvulsant. In addition, they are useful in screening
XX assays to identify small molecules that modulate or inhibit, for example,
XX neurogenesis, wound healing and angiogenesis. The nucleic acids are also

CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOXA protein
CC of the invention.
XX

Sequence 322 AA;

Query Match 95.5%; Score 322; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.9e-309; Indels 0; Gaps 0;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVAGTELTPTNGREETPCYKQTLSFTGTCIVSLVATLGNAAVLMILGCRMRNA 75
DB 1 MDSTIPVAGTELTPTNGREETPCYKQTLSFTGTCIVSLVATLGNAAVLMILGCRMRNA 60
QY 76 VSIYILNVADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
DB 61 VSIYILNVADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
QY 136 CLSIIMPWTWYHCRPRRYLSSVWCVLWALSLRSILTEWFCDFLFGSADSVWCETSDFT 195
DB 121 CLSIIMPWTWYHCRPRRYLSSVWCVLWALSLRSILTEWFCDFLFGSADSVWCETSDFT 180
QY 196 IAMLVFLCVLGGSLVLVLRILCGSRKMPRLRYVTLLTVLVFLGCLPGIOMALFS 255
DB 181 IAMLVFLCVLGGSLVLVLRILCGSRKMPRLRYVTLLTVLVFLGCLPGIOMALFS 240
QY 256 RIHLDKVLFCVHVLVSIFLSALNSSANPIIYFVGSFRORONKLVLRALQDTP 315
DB 241 RIHLDKVLFCVHVLVSIFLSALNSSANPIIYFVGSFRORONKLVLRALQDTP 300
QY 316 VDEGGWLPQETLELGSRL 337
DB 301 VDEGGWLPQETLELGSRL 322

RESULT 7

ABP81750
ID ABP81750 standard; protein, 322 AA.

AC ABP81750;

DT 04-MAR-2003 (first entry)

DE Human G protein-coupled receptor MrgX3 protein SEQ ID NO:674.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hyperextension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI: 2003-046718/04.

XX N-PSDB; AB242595.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (1) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, gratic versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcer, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
XX GPCR proteins given in ABP81675 to ABP81675, which are used in the
XX exemplification of the present invention

Sequence 322 AA;

Query Match 95.5%; Score 322; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.9e-309; Indels 0; Gaps 0;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVAGTELTPTNGREETPCYKQTLSFTGTCIVSLVATLGNAAVLMILGCRMRNA 75
DB 1 MDSTIPVAGTELTPTNGREETPCYKQTLSFTGTCIVSLVATLGNAAVLMILGCRMRNA 60
QY 76 VSIYILNVADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
DB 61 VSIYILNVADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
QY 136 CLSIIMPWTWYHCRPRRYLSSVWCVLWALSLRSILTEWFCDFLFGSADSVWCETSDFT 195
DB 121 CLSIIMPWTWYHCRPRRYLSSVWCVLWALSLRSILTEWFCDFLFGSADSVWCETSDFT 180
QY 196 IAMLVFLCVLGGSLVLVLRILCGSRKMPRLRYVTLLTVLVFLGCLPGIOMALFS 255
DB 181 IAMLVFLCVLGGSLVLVLRILCGSRKMPRLRYVTLLTVLVFLGCLPGIOMALFS 240
QY 256 RIHLDKVLFCVHVLVSIFLSALNSSANPIIYFVGSFRORONKLVLRALQDTP 315
DB 241 RIHLDKVLFCVHVLVSIFLSALNSSANPIIYFVGSFRORONKLVLRALQDTP 300
QY 316 VDEGGWLPQETLELGSRL 337
DB 301 VDEGGWLPQETLELGSRL 322

RESULT 8

ADH08535
ID ADH08535 standard; protein, 322 AA.

AC ADH08535;

DT 25-MAR-2004 (first entry)

DE MrGX3.
XX mas-related gene D; MrGD; Analgesic; Vulnerary; Ophthalmological;
KM sensory perception; glaucoma; MrG.
XX
OS Mus musculus.
XX WO2004003133-A1.
XX
XX 08-JAN-2004.
XX
XX 13-MAY-2003; 2003WO-US015004.
XX
XX 26-JUN-2002; 2002US-00183116.
XX
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Anderson DJ, Dong X, Zylka M, Han S, Simon MI;
XX WPI; 2004-083025/08.
XX N-PSDB; ADH08534.
XX
XX New mas-related gene D polypeptides, useful as therapeutics or in
XX identifying agonists or antagonists that alter pain perception in a
XX mammal for treating impaired sensory perception, e.g. chronic intractable
XX pain or neuropathic pain.
XX
XX
XX Disclosure; SEQ ID NO 31; 220pp; English.
XX
XX The present invention relates to an isolated mas-related gene D (MrGD)
XX polypeptide. The MrGD polypeptides are useful as therapeutics or for
XX identifying compounds, i.e. agonists or antagonists, that alter pain
XX perception in a mammal. The compounds are useful for treating impaired
XX sensory perception, e.g. chronic intractable pain or neuropathic pain,
XX promoting wound healing, restoring normal sensitivity following injury,
XX or treating ocular conditions, particularly those associated with
XX pressure such as glaucoma. The MrG genes or proteins may be used as
XX molecular probes for the detection of cells or tissues related to or
XX involved with sensory perception. The present sequence represents a MrGA
XX (MrG subfamily) protein.
XX
XX Sequence 322 AA;
SQ
Query Match 95.5%; Score 322; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.9e-309; Indels 0; Gaps 0;
Matches 322; Conservative 0; Mismatches 0;
QY 16 MDSTIPVLGTELPINGRETPCYKQTLSTFTGLTCTIVSLVATLGNVAVLMLGCRMRNA 75
DB 1 MDSTIPVLGTELPINGRETPCYKQTLSTFTGLTCTIVSLVATLGNVAVLMLGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 135
DB 61 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 120
QY 136 CLSIIMPPIWHCRPRYLSSVMCVLMLSLSLIEMMPCDPLFSGADSVWCETSDPT 195
DB 121 CLSIIMPPIWHCRPRYLSSVMCVLMLSLSLIEMMPCDPLFSGADSVWCETSDPT 180
QY 196 IAMLVFLCVLLCGSSLVLVRLICGSRKMPLTRLYTITLTVLVFLCGLPFGIQWALFS 255
DB 181 IAMLVFLCVLLCGSSLVLVRLICGSRKMPLTRLYTITLTVLVFLCGLPFGIQWALFS 240
QY 256 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSFRORONRKMLKVLORALDTPB 315
DB 241 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSFRORONRKMLKVLORALDTPB 300
QY 316 VDEGGGMLPOETTELSSGRLEQ 337
DB 301 VDEGGGMLPOETTELSSGRLEQ 322
RESULT 9

ADO44602
ID ADO44602 standard; protein; 322 AA.
XX
XX ADO44602;
AC
XX 29-JUL-2004 (first entry)
DE
XX Human HIT7213 protein.
XX
XX HIT7213; transgenic; G protein-coupled receptor; GPCR; ophthalmological;
XX cytostatic; nephrotoxic; antiinflammatory; dermatological; analgesic;
XX vulnerable; neuroprotective; human; receptor.
XX
XX Homo sapiens.
XX
XX WO2004039972-A1.
XX
XX 13-MAY-2004.
XX
XX 28-OCT-2003; 2003WO-JP013781.
XX
XX 29-OCT-2002; 2002JP-00314141.
XX
XX (TAKA) TAKEDA CHEM IND LTD.
XX
XX Kaisho Y, Watanabe T, Yasuhara Y, Mori I, Takeomi S;
XX WPI; 2004-376191/35.
XX N-PSDB; ADO44603.
XX
XX HIT7213 protein, encoded DNA and transgenic animals for clarifying
XX pathological mechanism, developing therapeutic methods and screening
XX preventives or remedies for related diseases e.g. cataract, cancer, and
XX dermatitis.
XX
XX
XX Claim 3; SEQ ID NO 1; 161pp; Japanese.
XX
XX The invention relates to a non-human mammal that carries a DNA integrated
XX with a foreign HIT7213 or its mutant gene, or a part of it. The non-human
XX animal is particularly a rat. Such gene shows phenotypes of e.g. cataract
XX onset, transient skin rash and proliferation-promoting activity. The
XX foreign HIT7213 gene is a gene that encodes a G protein-coupled receptor
XX (GPCR) protein HIT7213. The protein, its encoded DNA and constructed
XX transgenic animals are useful for clarifying pathological mechanism,
XX developing therapeutic methods and screening preventives or remedies for
XX related diseases e.g. cataract, cancer, and dermatitis. The present
XX sequence represents a human HIT7213 protein.
XX
XX Sequence 322 AA;
SQ
Query Match 95.5%; Score 322; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.9e-309; Indels 0; Gaps 0;
Matches 322; Conservative 0; Mismatches 0;
QY 16 MDSTIPVLGTELPINGRETPCYKQTLSTFTGLTCTIVSLVATLGNVAVLMLGCRMRNA 75
DB 1 MDSTIPVLGTELPINGRETPCYKQTLSTFTGLTCTIVSLVATLGNVAVLMLGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 135
DB 61 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 120
QY 136 CLSIIMPPIWHCRPRYLSSVMCVLMLSLSLIEMMPCDPLFSGADSVWCETSDPT 195
DB 121 CLSIIMPPIWHCRPRYLSSVMCVLMLSLSLIEMMPCDPLFSGADSVWCETSDPT 180
QY 196 IAMLVFLCVLLCGSSLVLVRLICGSRKMPLTRLYTITLTVLVFLCGLPFGIQWALFS 255
DB 181 IAMLVFLCVLLCGSSLVLVRLICGSRKMPLTRLYTITLTVLVFLCGLPFGIQWALFS 240
QY 256 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSFRORONRKMLKVLORALDTPB 315
DB 241 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSFRORONRKMLKVLORALDTPB 300

QY 316 VDEGGWLPQETLEISGRLEQ 337
 DB 301 VDEGGWLPQETLEISGRLEQ 322

RESULT 10
 ID ADO29705 standard; protein; 322 AA.
 XX ADO29705;
 AC ADO29705;
 XX 29-JUL-2004 (first entry)
 DT
 DE Human GPCR MRGX3, SEQ ID NO:807.
 XX
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KM transgenic mouse; neurological disorder; adrenal gland disorder;
 KM colon disorder; intestinal disorder; cardiovascular disorder;
 KM muscular disorder; blood disorder; immune disorder; bone disorder;
 KM joint disorder; metabolic disorder; nutritive disorder; cancer;
 KM kidney disorder; liver disorder; lung disorder; breast disorder;
 KM ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KM skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KM thymus disorder; thyroid disorder; antiparkinsonian; antitumor;
 KM cytoskeletal; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KM CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KM virocid; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KM dermatological; antitumor; antihypertensive; antidiabetic; antineoplastic;
 KM immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
 KM receptor.
 XX
 OS Homo sapiens.
 XX
 PN W02004040000-A2.
 PD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003WO-US0282226.
 XX
 PR 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 PA (PRIM-) PRIMAL INC.
 XX
 PI Galtanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li P;
 PI Medisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 DR WPI, 2004-390329/36.
 XX
 N-PSDB; ADO30080.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 XX Claim 151, SEQ ID NO 807; 542pp; English.
 XX
 XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a transgenic
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,

CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcr_sequences.
 XX
 SQ Sequence 322 AA;
 QY
 DB 16 MDSTIPVLTGTLTPNGEETPCYKQTLSEFGLCTIVSLVATGNVAVLWLGCRMRNA 75
 DB 1 MDSTIPVLTGTLTPNGEETPCYKQTLSEFGLCTIVSLVATGNVAVLWLGCRMRNA 60
 QY 76 VSIYILNVADPLFLSGHIIICSPRLINIRHPIKSLISPVMTPEYFGSMLSAISTER 135
 DB 61 VSIYILNVADPLFLSGHIIICSPRLINIRHPIKSLISPVMTPEYFGSMLSAISTER 120
 QY 136 CISTIPPIWHYCRPRRYISSVYVWLVWLSIRLSILEMFCDFLFGSADSVWCETSDPTT 195
 DB 121 CISTIPPIWHYCRPRRYISSVYVWLVWLSIRLSILEMFCDFLFGSADSVWCETSDPTT 180
 QY 196 IAMLVFLCVLTCSSIVLVVYILGSRKMPTRTYVTLITLVYFLCGIPGIGNALFS 255
 DB 181 IAMLVFLCVLTCSSIVLVVYILGSRKMPTRTYVTLITLVYFLCGIPGIGNALFS 240
 QY 256 RIHLDKVLFCVHLVSIIFLSALNSSANPIIYFVGSFRORONRMLKVLQBALDPTPE 315
 DB 241 RIHLDKVLFCVHLVSIIFLSALNSSANPIIYFVGSFRORONRMLKVLQBALDPTPE 300
 QY 316 VDEGGWLPQETLEISGRLEQ 337
 DB 301 VDEGGWLPQETLEISGRLEQ 322

RESULT 11
 ID ADF70481 standard; protein; 560 AA.
 XX ADF70481;
 AC ADF70481;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DB Orphan receptor ligand-related human protein SegID104.
 XX
 XX ligand; orphan receptor protein; fusion protein; fluorescent protein;
 KM cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
 KM GFPuv; Enhanced GFP; EGFP; human.
 XX
 OS Homo sapiens.
 XX
 PN W02003071272-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 21-FEB-2003; 2003WO-JP001901.
 XX
 PR 22-FEB-2002; 2002JP-00045728.
 PR 23-JUL-2002; 2002JP-00213949.
 PR 11-OCT-2002; 2002JP-00298237.

XX (TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX WPI; 2003-697654/66.
XX N-PSDB; ADF70583.
XX
XX Transformation of cells with a fusion protein of an orphan receptor
XX protein with a fluorescent protein useful for identification of ligands
XX to the orphan receptor.
XX
XX Disclosure; SEQ ID NO 104; 594pp; Japanese.
XX
XX This invention relates to a novel method of identifying ligands to an
XX orphan receptor protein which comprises transforming cells with DNA
XX encoding a fusion protein of the orphan receptor with a fluorescent
XX protein, so that the fusion protein is expressed in the cells (or cell
XX membranes isolated from them) and contacting the cells with the potential
XX ligand to be tested. A suitable fluorescent protein for incorporation in
XX the fusion protein is green fluorescent protein (GFP), for example GFP-1,
XX wild-type GFP, GFPuv or enhanced GFP (EGFP). The method is useful for the
XX identification of ligands binding to an orphan receptor protein.
XX
XX Sequence 560 AA;
SQ
Query Match 95.5%; Score 322; DB 7; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.9e-309; Indels 0; Gaps 0;
Matches 322; Conservative 0; Mismatches 0;
QY 16 MDSTIPVLGTELPINGREETPCYKOTLSTFGTLCIYSLVALNGNAVWMLGCRMRNA 75
DB 1 MDSTIPVLGTELPINGREETPCYKOTLSTFGTLCIYSLVALNGNAVWMLGCRMRNA 60
QY 76 VSIYIINLVADFLPSGHIICSPRLINIRHPISKLSVMTPTPYFGLSMTSAISTER 135
DB 61 VSIYIINLVADFLPSGHIICSPRLINIRHPISKLSVMTPTPYFGLSMTSAISTER 120
QY 136 CSTIIPWYHCRPRYLSSVWCYLWALSLRSTLEMMPCDPLFSGADSWCETSDFIT 195
DB 121 CSTIIPWYHCRPRYLSSVWCYLWALSLRSTLEMMPCDPLFSGADSWCETSDFIT 180
QY 196 IAWLVPLCVLCCSSLVLVRIILGSRKMPRLRYVTLLTVLVFLGCLPFGIOWALFS 255
DB 181 IAWLVPLCVLCCSSLVLVRIILGSRKMPRLRYVTLLTVLVFLGCLPFGIOWALFS 240
QY 256 RIHLDMKVLFCCHVLVSIPLSALNSSANPIIYFVGSFRQRONRKIKVLQRALQDTPR 315
DB 241 RIHLDMKVLFCCHVLVSIPLSALNSSANPIIYFVGSFRQRONRKIKVLQRALQDTPR 300
QY 316 VDEGGGMLPQETLELSSRLQ 337
DB 301 VDEGGGMLPQETLELSSRLQ 322
RESULT 12
ADP29105
ID ADF29105 standard; protein; 322 AA.
AC ADF29105;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human GPCR R-14.
XX
XX Human; R-14; GPCR; G protein coupled receptor;
XX trabecular meshwork tissue; ocular outflow; antagonist;
XX ocular hypotensive; drug screening; elevated intraocular pressure;
XX glaucoma; ophthalmological; receptor.
XX
XX Homo sapiens.
XX
XX WO2003080659-A1.

XX 02-OCT-2003.
XX
XX 27-MAR-2003; 2003WO-CA000444.
XX
XX 27-MAR-2002; 2002US-0367513P.
XX
XX (THER-) THERATECHNOLOGIES INC.
XX
XX Peri KG, Mofelt S, Abran D;
XX
XX WPI; 2004-053019/05.
XX N-PSDB; ADF29104.
XX
XX New substantially pure R-14 polypeptide, useful as drug targets for
XX lowering intraocular pressure and for treating condition such as
XX glaucoma.
XX
XX Claim 21; SEQ ID NO 2; 85pp; English.
XX
XX The invention relates to a human GPCR (G protein coupled receptor)
XX designated R-14 (ADP29105), nucleic acids encoding it (ADP29104), and R-
XX 14 peptide antagonists (ADP29106-ADP29108). The invention also
XX encompasses vectors and host cells comprising R-14 nucleic acids, and
XX methods of screening for R-14 antagonists. The R-14 receptor is expressed
XX in trabecular meshwork tissue, and is associated with a role in ocular
XX outflow. Inhibition of the receptor results in a reduction of basal
XX intraocular pressure, making the R-14 receptor a useful target for
XX screening for ocular hypotensive drugs. The R-14 peptide antagonists are
XX useful for reducing intraocular pressure for the treatment of conditions
XX associated with elevated intraocular pressure such as glaucoma and
XX related conditions. The R-14 receptor, and host cells expressing an R-14
XX polynucleotide, may be used in screening for R-14 receptor antagonists.
XX The present sequence is related to the invention.
XX
XX Sequence 322 AA;
SQ
Query Match 82.2%; Score 277; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.6e-265; Indels 0; Gaps 0;
Matches 277; Conservative 0; Mismatches 0;
QY 61 AVVLMILGCRMRNAVSIYILNLVADFLPSGHIICSPRLINIRHPISKLSVMTPTFP 120
DB 46 AVVLMILGCRMRNAVSIYILNLVADFLPSGHIICSPRLINIRHPISKLSVMTPTFP 105
QY 121 YFGLSMTLSAISTERCLSTIMPWYHCRPRYLSSVWCYLWALSLRSTLEMMPCDPLF 180
DB 106 YFGLSMTLSAISTERCLSTIMPWYHCRPRYLSSVWCYLWALSLRSTLEMMPCDPLF 165
QY 181 SGADSVWCETSDFITIAMLVFLCVLCCSSLVLVRIILGSRKMPRLRYVTLLTVLVF 240
DB 166 SGADSVWCETSDFITIAMLVFLCVLCCSSLVLVRIILGSRKMPRLRYVTLLTVLVF 225
QY 241 ILGCLPFGIOWALFSRIHLDMKVLFCCHVLVSIPLSALNSSANPIIYFVGSFRQRONRQ 300
DB 226 ILGCLPFGIOWALFSRIHLDMKVLFCCHVLVSIPLSALNSSANPIIYFVGSFRQRONRQ 285
QY 301 NLKLVQLQALQDTPRVDGEGGMLPQETLELSSRLQ 337
DB 286 NLKLVQLQALQDTPRVDGEGGMLPQETLELSSRLQ 322
RESULT 13
AAB14846
ID AAB14846 standard; protein; 322 AA.
AC AAB14846;
XX
XX 19-DEC-2000 (first entry)
XX
XX Human novel G-protein coupled receptor #1.
XX
XX Human; novel G-protein coupled receptor; signal transduction;
XX

KW disease diagnosis; drug screening; disease therapy.
XX Homo sapiens.
XX WO200040724-A1.
XX
XX 13-JUL-2000.
XX
XX 04-JAN-2000; 2000WO-US000052.
XX
XX 04-JAN-1999; 99US-0114666P.
PR 14-JAN-1999; 99US-0115828P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Nehls M, Wattler F;
XX WPI; 2000-465986/40.
DR N-PSDB; AAA70342.
XX
XX New polynucleotides encoding novel G-protein coupled receptors useful for
PT diagnosis, drug screening, clinical trial monitoring and for the
PT treatment of physiological or behavioral disorders.
XX
XX Claim 1; Page 53-54; 61pp; English.
XX
XX The present sequence is the protein sequence for a novel human G-protein
CC coupled receptor (NGPCR). These proteins are involved in signal
CC transduction pathways in many cases. The protein contains seven
CC transmembrane domains, and is expressed in human testis, mammary gland
CC and salivary gland tissue. The protein, its gene, agonists, antagonists
CC and antibodies can be used to diagnose and treat diseases associated with
CC the inappropriate expression or expression of mutant versions of the
CC protein, for screening for drugs which can be used in the same manner,
CC and for elucidating the function of the protein
XX
XX Sequence 322 AA;
SQ
Query Match 66.5%; Score 224; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.1e-212;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 SPLRLINRHPISKLSVMTFPYFGISMSAISTERCLSLMPVHCRPRYLSVM 157
DB 83 SPLRLINRHPISKLSVMTFPYFGISMSAISTERCLSLMPVHCRPRYLSVM 142
QY 158 CVLLMALSLRSILSEMFCDPLFSGADSVWCETSDPTITAMLVFLCVLTCSSVLVARI 217
DB 143 CVLLMALSLRSILSEMFCDPLFSGADSVWCETSDPTITAMLVFLCVLTCSSVLVARI 202
QY 218 LCGSRKMPRLRYVITLTVLVEFLCGLPFGIQMALFSRIHDMKVLFCVHVLVSIPLSA 277
DB 203 LCGSRKMPRLRYVITLTVLVEFLCGLPFGIQMALFSRIHDMKVLFCVHVLVSIPLSA 262
QY 278 LNSSANPIYFVGSFRORONRQNLKVLQRALODTPEVDEGGG 321
DB 263 LNSSANPIYFVGSFRORONRQNLKVLQRALODTPEVDEGGG 306
RESULT 14
AA90762
ID AAY90762 standard; protein; 322 AA.
XX
XX AAY90762;
XX
XX 18-AUG-2000 (first entry)
XX
XX Human G protein-coupled receptor hHR77213V SEQ ID NO:2.
XX
XX Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
KM genetic disease; cellular function regulation.
XX
OS Homo sapiens.

XX
XX WO200020455-A1.
XX
XX 13-APR-2000.
XX
XX 30-SEP-1999; 99WO-JP005366.
XX
XX 01-OCT-1998; 98JP-00279535.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Watanabe T, Terao Y, Matsui H;
XX WPI; 2000-303747/26.
DR N-PSDB; AAA29812.
XX
XX Human-derived G protein-coupled protein and encoding nucleic acid, useful
PT e.g. in determining ligands and treatment of diseases associated with
PT dysfunction of the protein.
XX
XX Claim 2; Page 92-93; 97pp; Japanese.
XX
XX The present sequence represents a human-derived G protein-coupled protein
CC designated hHR77213V, which is isolated from the human hippocampus. The G
CC protein-coupled receptor can be used for preventing, treating and
CC diagnosing genetic diseases associated with G protein-coupled protein,
CC and for regulating cellular functions. The protein can be used to prevent
CC and treat disorders associated with G protein-coupled protein gene
CC dysfunction. It can also be used to identify G protein-coupled protein
CC ligands and generating antibodies and antisera against the protein. It is
CC also useful in constructing recombinant receptor protein expression
CC systems, developing receptor-binding assay systems and screening drug
CC candidates, and can be used as a probe in the genetic diagnosis of G
CC protein-coupled protein disorders
XX
XX Sequence 322 AA;
SQ
Query Match 65.6%; Score 221; DB 3; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.9e-209;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 MDSTIPVGTGLTPNGRETPCYKQTLSPFGLTCIVSLVATGNNAVVLGCRMRNA 75
DB 1 MDSTIPVGTGLTPNGRETPCYKQTLSPFGLTCIVSLVATGNNAVVLGCRMRNA 60
QY 76 VSIYILNVADPLFLSGHITCSPLRLINRHPISKLSVMTFPYFGISMSAISTER 135
DB 61 VSIYILNVADPLFLSGHITCSPLRLINRHPISKLSVMTFPYFGISMSAISTER 120
QY 136 CLSLMPVHCRPRYLSVMCVLLMALSLRSILSEMFCDPLFSGADSVWCETSDPT 195
DB 121 CLSLMPVHCRPRYLSVMCVLLMALSLRSILSEMFCDPLFSGADSVWCETSDPT 180
QY 196 IAMLVFLCVLTCSSVLVARIILCGSRKMPRLRYVITLTVLVEFLCGLPFGIQMALFS 255
DB 181 IAMLVFLCVLTCSSVLVARIILCGSRKMPRLRYVITLTVLVEFLCGLPFGIQMALFS 240
QY 256 RIHDMKVLFCVHVLVSIPLSALNSSANPIYFVGSFRORONRQNLKVLQRALODTPE 315
DB 241 RIHDMKVLFCVHVLVSIPLSALNSSANPIYFVGSFRORONRQNLKVLQRALODTPE 300
QY 316 VDEGGWLPQETLEISGRLEQ 337
DB 301 VDEGGWLPQETLEISGRLEQ 322
RESULT 15
AD16994
ID AD16994 standard; protein; 322 AA.
XX
XX AD16994;
XX
XX 15-APR-2004 (first entry)
XX
XX

XX Human NOVX protein homologue SeqID 530.
DE human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.
XX Homo sapiens.
OS
PN MO200268649-A2.
PD 06-SEP-2002.
XX
XX 31-JAN-2002; 2002MO-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 08-FEB-2001; 2001US-0267057P.
XX 09-FEB-2001; 2001US-0267459P.
XX 15-FEB-2001; 2001US-0267833P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276377P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0279862P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282992P.
XX 20-APR-2001; 2001US-0283083P.
XX 23-APR-2001; 2001US-0285133P.
XX 03-MAY-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 29-MAY-2001; 2001US-0288504P.
XX 30-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296964P.
XX 18-JUN-2001; 2001US-0298959P.
XX 13-JUN-2001; 2001US-0299324P.
XX 15-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312908P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.
XX 31-AUG-2001; 2001US-0316447P.
XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318118P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323379P.
XX 18-OCT-2001; 2001US-0320245P.
XX 18-OCT-2001; 2001US-0330308P.
XX 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.

XX
PI Tchernev VT, Spytek KA, Zernhusen BD, Patuturajan M, Shinkets RA;
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CR; CB;
PI Futrak K, Grosse WM, Alsdbrook JP, Lepley DM, Rieger DK, Burgess CB;
XX WPI; 2002-706998/76.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, or
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Disclosure; SEQ ID NO 530; 1498bp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy,
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC hemostatic, anti-HIV, antidiabetic, antirheumatic, anorectic,
CC neurostimulant, neurotropic, anticholinergic, hepatotropic,
CC autostimulant, neuropeptide, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.
XX
XX Sequence 322 AA;
SQ
Query Match 65.6%; Score 221; DB 5; Length 322;
Best Local Similarity 99.7%; Pred. No. 1.9e-209;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 MDSTIPVLTGTELPINGREBETPCYKOTLSFTGTCIVSLVATLGNVVLMLGCRMRNA 75
DB 1 MDSTIPVLTGTELPINGREBETPCYKOTLSFTGTCIVSLVATLGNVVLMLGCRMRNA 60
QY 76 VSIYIINLVADPLFLSGHICSPRLINIRHDSKILSPVMTFPYIGISMLSAISTER 135
DB VSIYIINLVADPLFLSGHICSPRLINIRHDSKILSPVMTFPYIGISMLSAISTER 120
QY 61 VSIYIINLVADPLFLSGHICSPRLINIRHDSKILSPVMTFPYIGISMLSAISTER 120
DB VSIYIINLVADPLFLSGHICSPRLINIRHDSKILSPVMTFPYIGISMLSAISTER 120
QY 136 CLSILMPPIWYHCRPRYLSSVWCVLMLALSILSIEMFCDPLFGANSVWCETSDFIT 155
DB CLSILMPPIWYHCRPRYLSSVWCVLMLALSILSIEMFCDPLFGANSVWCETSDFIT 180
QY 121 CLSILMPPIWYHCRPRYLSSVWCVLMLALSILSIEMFCDPLFGANSVWCETSDFIT 180
DB CLSILMPPIWYHCRPRYLSSVWCVLMLALSILSIEMFCDPLFGANSVWCETSDFIT 180
QY 196 IAWLVFLCVLTCSSSVLVLVRLICGSRKMPLTLYTTLTVVAVFLGCPFGIOWALFS 255
DB IAWLVFLCVLTCSSSVLVLVRLICGSRKMPLTLYTTLTVVAVFLGCPFGIOWALFS 240
QY 181 IAWLVFLCVLTCSSSVLVLVRLICGSRKMPLTLYTTLTVVAVFLGCPFGIOWALFS 240
DB IAWLVFLCVLTCSSSVLVLVRLICGSRKMPLTLYTTLTVVAVFLGCPFGIOWALFS 240
QY 256 RIHLDKRVLECHVHLVSIPLSALNSSANPIYFVGSFRQRQRNMLKVLQRLQDTPS 315
DB RIHLDKRVLECHVHLVSIPLSALNSSANPIYFVGSFRQRQRNMLKVLQRLQDTPS 300
QY 241 RIHLDKRVLECHVHLVSIPLSALNSSANPIYFVGSFRQRQRNMLKVLQRLQDTPS 300
DB RIHLDKRVLECHVHLVSIPLSALNSSANPIYFVGSFRQRQRNMLKVLQRLQDTPS 300
QY 316 VDEGGGMLPQETLELSGSRLEQ 337
DB VDEGGGMLPQETLELSGSRLEQ 322

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Page 12

Search completed: October 27, 2004, 08:48:14
Job time : 156 secs

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; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-5

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Query Match          25.5%; Score 86; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.5e-74;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 204 VLGGSSIVLVRLICGSRKMPRLVYTIITLVVFLICGIPFGIOWALPSRIHLDKRV 263
DB 189 VLICGSSIVLVRLICGSRKMPRLVYTIITLVVFLICGIPFGIOWALPSRIHLDKRV 248
QY 264 LFCVHLVSIPLSALNSSANPIIYF 289
DB 249 LFCVHLVSIPLSALNSSANPIIYF 274

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RESULT 3
US-09-254-227A-9
; Sequence 9, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-9

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Query Match          14.8%; Score 50; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 263 VLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQRALOD 312
DB 248 VLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQRALOD 297

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RESULT 4

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US-09-254-227A-7
; Sequence 7, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03

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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-7

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Query Match          13.1%; Score 44; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.4e-34;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 294 RORORONRQNLKVLQRALODTPEVDGSGWLPQFTLEISGRLRQ 337
DB 279 RORORONRQNLKVLQRALODTPEVDGSGWLPQFTLEISGRLRQ 322

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RESULT 5
US-09-254-227A-11
; Sequence 11, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-11

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Query Match          12.2%; Score 41; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.2e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 209 SSVLVVRLICGSRKMPRLVYTIITLVVFLICGIPFGI 249
DB 194 SSVLVVRLICGSRKMPRLVYTIITLVVFLICGIPFGI 234

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RESULT 6
US-09-254-227A-13
; Sequence 13, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-13

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Query Match 12.2%; Score 41; DB 4; Length 322;

Best Local Similarity 100.0%; Pred. No. 6.2e-31;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 SSIVLVRIICGSRKMPITLVYITLTIVVPLICGIPFgi 249
Db 194 SSIVLVRIICGSRKMPITLVYITLTIVVPLICGIPFgi 234

RESULT 7

US-09-254-227A-1
; Sequence 1, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Portin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRT
; ORGANISM: rat
US-09-254-227A-1

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Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 LSAISTERCLS 138
Db 131 LSAISTERCLS 141

RESULT 8

US-09-489-039A-10936
; Sequence 10936, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10936
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10936

Query Match 3.0%; Score 10; DB 4; Length 773;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 VSIFLSALNS 280
Db 523 VSIFLSALNS 532

RESULT 9
US-09-255-368-8
; Sequence 8, Application US/09255368
; Patent No. 6262246

; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.

; APPLICANT: Borowsky, Beth
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide RF (NPFF) Receptors
; FILE REFERENCE: 1795/57155-A
; CURRENT APPLICATION NUMBER: US/09/255,368
; CURRENT FILING DATE: 1999-02-22
; EARLIER APPLICATION NUMBER: 09/161,113
; EARLIER FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0 - beta
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-255-368-8

Query Match 2.7%; Score 9; DB 3; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 NSSANPIIY 287
Db 321 NSSANPIIY 329

RESULT 10

US-09-405-558-8
; Sequence 8, Application US/09405558A
; Patent No. 6709831
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide RF (NPFF) Receptors
; FILE REFERENCE: 57155-C
; CURRENT APPLICATION NUMBER: US/09/405,558A
; CURRENT FILING DATE: 1999-09-24
; EARLIER APPLICATION NUMBER: 09/161,113
; EARLIER FILING DATE: 1998-09-25
; EARLIER APPLICATION NUMBER: 09/255,368
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin Ver. 2.0 - beta
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-405-558-8

Query Match 2.7%; Score 9; DB 4; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 NSSANPIIY 287
Db 321 NSSANPIIY 329

RESULT 11

US-08-978-404B-31
; Sequence 31, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN

NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5968782e
US-08-978-404B-31

Query Match 2.4%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 LLMALSL 167
DB 8 LLMALSL 15

RESULT 12
US-09-016-366A-15
Sequence 15, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-366A-15

Query Match 2.4%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 LLMALSL 167
DB 8 LLMALSL 15

RESULT 13
US-08-978-404B-21
Sequence 21, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5968782e
US-08-978-404B-21

Query Match 2.4%; Score 8; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 LLMALSIL 167
 Db 8 LLMALSIL 15

RESULT 14
 US-09-134-001C-3801
 ; Sequence 3801, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3801
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3801

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 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 WLPQETLE 329
 Db 79 WLPQETLE 86

RESULT 15
 US-09-255-368-2
 ; Sequence 2, Application US/09255368
 ; Patent No. 6262246
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerald, Christophe P.G.
 ; APPLICANT: Jones, Kenneth A.
 ; APPLICANT: Bonini, James A.
 ; APPLICANT: Borowsky, Beth
 ; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
 ; FILE REFERENCE: 1795/57155-A
 ; CURRENT APPLICATION NUMBER: US/09/255,368
 ; CURRENT FILING DATE: 1999-02-22
 ; EARLIER APPLICATION NUMBER: 09/161,113
 ; EARLIER FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patent Ver. 2.0 - beta
 ; SEQ ID NO 2
 ; LENGTH: 432
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-255-368-2

Query Match 2.4%; Score 8; DB 3; Length 432;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 SSANPIY 287
 Db 324 SSANPIY 331

Search completed: October 27, 2004, 08:52:22
 Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2004, 08:51:45 / Search time 132 Seconds
(without alignments)
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Title: US-09-867-570-2

Sequence: 1 MESKSSWVIRLGLSDSTI.....EGGGMLPQTLRLSGRLBQ 337

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Searched: 1370721 seqs, 324215800 residues

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337	100.0	337	11	US-09-867-570-2
2	332	95.5	332	9	US-09-995-225-20
3	332	95.5	332	10	US-09-995-225-20
4	332	95.5	332	14	US-10-183-116-31
5	332	95.5	332	14	US-10-225-567A-674
6	332	95.5	332	14	US-10-072-012-529
7	332	95.5	332	15	US-10-072-012-534
8	332	95.5	332	14	US-10-219-834-79
9	332	95.5	332	14	US-10-401-397A-2
10	332	95.5	332	14	US-10-391-074-2
11	332	95.5	332	15	US-10-292-798-1274
12	332	95.5	332	15	US-10-072-012-530
13	332	95.5	332	15	US-10-072-012-535

14	181	53.7	302	14	US-10-237-467-10	Sequence 10, Appl
15	131	38.9	197	14	US-10-017-161-1600	Sequence 1600, Ap
16	76	22.6	76	14	US-10-219-834-174	Sequence 174, App
17	76	22.6	328	14	US-10-219-834-20	Sequence 20, Appl
18	50	14.8	319	15	US-10-072-012-174	Sequence 174, App
19	50	14.8	332	14	US-10-183-116-16	Sequence 16, Appl
20	50	14.8	332	14	US-10-079-384-4	Sequence 4, Appl1
21	50	14.8	332	14	US-10-017-161-1056	Sequence 1056, Ap
22	50	14.8	332	14	US-10-240-998-4	Sequence 4, Appl1
23	50	14.8	332	14	US-10-321-807-20	Sequence 20, Appl
24	50	14.8	332	14	US-10-237-467-12	Sequence 12, Appl
25	50	14.8	332	14	US-10-292-798-898	Sequence 898, App
26	50	14.8	332	15	US-10-016-248-81	Sequence 81, Appl
27	50	14.8	332	15	US-10-072-012-172	Sequence 172, App
28	50	14.8	332	15	US-10-072-012-527	Sequence 527, App
29	50	14.8	332	15	US-10-072-012-533	Sequence 533, App
30	50	14.8	332	15	US-10-343-650A-44	Sequence 44, Appl
31	50	14.8	332	16	US-10-321-807-20	Sequence 20, Appl
32	50	14.8	332	16	US-10-314-048A-20	Sequence 20, Appl
33	50	14.8	1589	15	US-10-072-012-528	Sequence 528, App
34	50	14.8	1589	15	US-10-072-012-532	Sequence 532, App
35	41	12.2	176	14	US-10-116-252-11	Sequence 11, Appl
36	41	12.2	322	9	US-09-995-225-18	Sequence 18, Appl
37	41	12.2	322	10	US-09-995-225-18	Sequence 18, Appl
38	41	12.2	332	14	US-10-183-116-33	Sequence 33, Appl
39	41	12.2	332	14	US-10-225-567A-689	Sequence 689, App
40	41	12.2	332	14	US-10-237-467-4	Sequence 4, Appl1
41	41	12.2	332	14	US-10-292-798-1042	Sequence 1042, Ap
42	41	12.2	332	15	US-10-016-248-84	Sequence 84, Appl
43	41	12.2	332	15	US-10-072-012-531	Sequence 531, App
44	41	12.2	332	15	US-10-072-012-536	Sequence 536, App
45	30	8.9	319	15	US-10-072-012-170	Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-867-570-2
Sequence 2, Application US/09867570
Publication No. US20040076951A1
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000900-CIP
CURRENT APPLICATION NUMBER: US/09/867,570
CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/695,045
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 337
TYPE: PRT
ORGANISM: Human
US-09-867-570-2

Query Match 100.0%; Score 337; DB 11; Length 337;
Best Local Similarity 100.0%; Pred. No. 4, 1e-300;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESKSSWVIRLGLSDSTIPIVGTETIPNGEBEPYKQTLSPFGLTCTIVSVALTGN 60
DB 1 MESKSSWVIRLGLSDSTIPIVGTETIPNGEBEPYKQTLSPFGLTCTIVSVALTGN 60
QY 61 AAVLMLGCMRBNNAVSIYTLNVAADPLFLSHIICSPRLINIRIPISKIISPWTFF 120
DB 61 AAVLMLGCMRBNNAVSIYTLNVAADPLFLSHIICSPRLINIRIPISKIISPWTFF 120
QY 121 YFTGLSTSAISTERCISITPIWYHQRBRYSVWCVLMLALSLRSLILEMFCDFLF 180
DB 121 YFTGLSTSAISTERCISITPIWYHQRBRYSVWCVLMLALSLRSLILEMFCDFLF 180

Db 121 YFGLSMLSAISTERCISILMPWYHCRPRYLSSVMCVLLMALSLRSILEMFCDFLE 180
Qy 181 SGADSWCETSDFTITAMVFLCVVLICGSSLVLVIRILCGSRKMPLTRLYTITLTVLVE 240
Db 181 SGADSWCETSDFTITAMVFLCVVLICGSSLVLVIRILCGSRKMPLTRLYTITLTVLVE 240
Qy 241 LCGLPFGIOWALFSRHLDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQ 300
Db 241 LCGLPFGIOWALFSRHLDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQ 300
Qy 301 NKLVLQALODTPEVDEGGGMLPOETLEISGSRLEQ 337
Db 301 NKLVLQALODTPEVDEGGGMLPOETLEISGSRLEQ 337

RESULT 2

US-09-995-225-20
Sequence 20, Application US/09995225
Publication No. US20020193584A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Priddy, Cameron
TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,365
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,032
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/290,917
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 322
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US20020193584A1 Sequence
US-09-995-225-20

Query Match 95.5%; Score 322; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.2e-286;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MDSTIPVLGTELTPTINGREETPCYKQTLSPFGLTCTIVSLVATGNAVVLMLGCMRRNA 75
Db 1 MDSTIPVLGTELTPTINGREETPCYKQTLSPFGLTCTIVSLVATGNAVVLMLGCMRRNA 60
Qy 76 VSIYILNLVADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135

Db 61 VSIYILNLVADFLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Qy 136 CISTIMPIWYHCRPRYLSSVMCVLLMALSLRSILEMFCDFLESGADSWCETSDFT 195
Db 121 CISTIMPIWYHCRPRYLSSVMCVLLMALSLRSILEMFCDFLESGADSWCETSDFT 180
Qy 196 IAMVFLCVVLICGSSLVLVIRILCGSRKMPLTRLYTITLTVLVEFLLGSLPFGIOWALFS 255
Db 181 IAMVFLCVVLICGSSLVLVIRILCGSRKMPLTRLYTITLTVLVEFLLGSLPFGIOWALFS 240
Qy 256 RIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQALODTPE 315
Db 241 RIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQALODTPE 300
Qy 316 VDEGGGMLPOETLEISGSRLEQ 337
Db 301 VDEGGGMLPOETLEISGSRLEQ 322

RESULT 3

US-09-995-225-20
Sequence 20, Application US/09995225
Publication No. US20030139588A9
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Priddy, Cameron
TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/09/995,225
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,365
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,032
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/290,917
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 322
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US20030139588A9 Sequence
US-09-995-225-20

Query Match 95.5%; Score 322; DB 10; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.2e-286;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELTPIINGREBETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMILGCRMRNA 75
DB 1 MDSTIPVLGTELTPIINGREBETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMILGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 135
DB 61 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 120
QY 136 CTSILMPIMWCHCRPRYLSSVMCVLMLALSILRSILEMFCDFLFGADSVWCETSDFIT 195
DB 121 CTSILMPIMWCHCRPRYLSSVMCVLMLALSILRSILEMFCDFLFGADSVWCETSDFIT 180
QY 196 IAMLVFLCVLLCGSSVLVLVRLICGSRKMPLTRLYVTYITLLTVLVFLLCGIPFGIQWALFS 255
DB 181 IAMLVFLCVLLCGSSVLVLVRLICGSRKMPLTRLYVTYITLLTVLVFLLCGIPFGIQWALFS 240
QY 256 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSSFRORONRQMLKVLQALODTPE 315
DB 241 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSSFRORONRQMLKVLQALODTPE 300
QY 316 VDEGGGMLPOETLELSGRLEQ 337
DB 301 VDEGGGMLPOETLELSGRLEQ 322

RESULT 4

US-10-183-116-31
; Sequence 31, Application US/10183116
; Publication No. US2003092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylke, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-Kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4CICP1
; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-183-116-31

Query Match 95.5%; Score 322; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.2e-286;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELTPIINGREBETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMILGCRMRNA 75
DB 1 MDSTIPVLGTELTPIINGREBETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMILGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 135
DB 61 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 120
QY 136 CTSILMPIMWCHCRPRYLSSVMCVLMLALSILRSILEMFCDFLFGADSVWCETSDFIT 195
DB 121 CTSILMPIMWCHCRPRYLSSVMCVLMLALSILRSILEMFCDFLFGADSVWCETSDFIT 180

QY 196 IAMLVFLCVLLCGSSVLVLVRLICGSRKMPLTRLYVTYITLLTVLVFLLCGIPFGIQWALFS 255
DB 181 IAMLVFLCVLLCGSSVLVLVRLICGSRKMPLTRLYVTYITLLTVLVFLLCGIPFGIQWALFS 240
QY 256 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSSFRORONRQMLKVLQALODTPE 315
DB 241 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSSFRORONRQMLKVLQALODTPE 300
QY 316 VDEGGGMLPOETLELSGRLEQ 337
DB 301 VDEGGGMLPOETLELSGRLEQ 322

RESULT 5

US-10-225-567A-674
; Sequence 674, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 674
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-674

Query Match 95.5%; Score 322; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.2e-286;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELTPIINGREBETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMILGCRMRNA 75
DB 1 MDSTIPVLGTELTPIINGREBETPCYKOTLSFTGLTCTIVSLVATLGNNAVLMILGCRMRNA 60
QY 76 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 135
DB 61 VSIYIINLVAAADFLPSGHIICSPRLINIRHPISKILSPVMTFPYFIGLSMISAISTER 120
QY 136 CTSILMPIMWCHCRPRYLSSVMCVLMLALSILRSILEMFCDFLFGADSVWCETSDFIT 195
DB 121 CTSILMPIMWCHCRPRYLSSVMCVLMLALSILRSILEMFCDFLFGADSVWCETSDFIT 180
QY 196 IAMLVFLCVLLCGSSVLVLVRLICGSRKMPLTRLYVTYITLLTVLVFLLCGIPFGIQWALFS 255
DB 181 IAMLVFLCVLLCGSSVLVLVRLICGSRKMPLTRLYVTYITLLTVLVFLLCGIPFGIQWALFS 240
QY 256 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSSFRORONRQMLKVLQALODTPE 315
DB 241 RIHLDMKVLFCFVHLVSIPLSALNSSANPIIYFVGSSFRORONRQMLKVLQALODTPE 300
QY 316 VDEGGGMLPOETLELSGRLEQ 337
DB 301 VDEGGGMLPOETLELSGRLEQ 322

RESULT 6

US-10-072-012-529
; Sequence 529, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tcheurnev, Velizar
; APPLICANT: Spytsek, Kimberly
; APPLICANT: Zerhusen, Bryan

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/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 529
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-529

Query Match          95.5%; Score 322; DB 15; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.2e-286;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MDSTIPVLGTELTPTINGREETPCYKQTSFTGLTCTIVSLVALTGNAVVMILGCMRRNA 75
DB 1 MDSTIPVLGTELTPTINGREETPCYKQTSFTGLTCTIVSLVALTGNAVVMILGCMRRNA 60

QY 76 VSIYIILNVAADPLFLSGHIIICSPRLINIRHPISKIISPVTFFPYFGLSMLSAISTER 135
DB 61 VSIYIILNVAADPLFLSGHIIICSPRLINIRHPISKIISPVTFFPYFGLSMLSAISTER 120

QY 136 CLSTIMPWYHCRPRRYSSVWCVLMLSLSLSTLSEWMPGDFLSSGADSVWCETSDFT 195
DB 121 CLSTIMPWYHCRPRRYSSVWCVLMLSLSLSTLSEWMPGDFLSSGADSVWCETSDFT 180

QY 196 IAWIVPLCVVCGSSSLVLLVRLICSSRKXPLTRLVYVTLITLVVFLGCLPGGIOMALFS 255
DB 181 IAWIVPLCVVCGSSSLVLLVRLICSSRKXPLTRLVYVTLITLVVFLGCLPGGIOMALFS 240
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QY 256 RIHDMKVLFGHYLVSTFLSALNSSANPITTFVGSFRORONRNLKVLORALDTPPE 315
DB 241 RIHDMKVLFGHYLVSTFLSALNSSANPITTFVGSFRORONRNLKVLORALDTPPE 300

QY 316 VDEGGMLPORTLEISGSRLSEQ 337
DB 301 VDEGGMLPORTLEISGSRLSEQ 322

RESULT 7
US-10-072-012-534
/ Sequence 534, Application US/10072012
/ Publication No. US20040033493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 534
/ LENGTH: 322
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-534

Query Match          95.5%; Score 322; DB 15; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.2e-286;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 16 MDSTIPVLGTELTPINGREERTPCYKOTLSFTGLTCIVSLVATGNVAVLMLGCRMRNA 75
Db 1 MDSTIPVLGTELTPINGREERTPCYKOTLSFTGLTCIVSLVATGNVAVLMLGCRMRNA 60
Qy 76 VSIYIILNLVAADPLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
Db 61 VSIYIILNLVAADPLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Qy 136 CUSIIMPIMWHCRPRRLSSVMCVLMLALSILSLIEMMCDPLFGSADSVWCETSDPIT 155
Db 121 CUSIIMPIMWHCRPRRLSSVMCVLMLALSILSLIEMMCDPLFGSADSVWCETSDPIT 180
Qy 196 IAMLVPLCVLCCSSSLVLRILGSRKMPRLRYTITLTVLVLGCLPFGIQMALFS 255
Db 181 IAMLVPLCVLCCSSSLVLRILGSRKMPRLRYTITLTVLVLGCLPFGIQMALFS 240
Qy 256 RIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQRALQDTPR 315
Db 241 RIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQRALQDTPR 300
Qy 316 VDEGGGWLPOETLESGSRLEQ 337
Db 301 VDEGGGWLPOETLESGSRLEQ 322

RESULT 8

US-10-219-834-79
; Sequence 79, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219, 834
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313,658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340,703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318,675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355,596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333,417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338,367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-79

Query Match 85.2%; Score 287; DB 14; Length 314;

Best Local Similarity 100.0%; Pred. No. 2,4e-254;

Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MDSTIPVLGTELTPINGREERTPCYKOTLSFTGLTCIVSLVATGNVAVLMLGCRMRNA 75
Db 1 MDSTIPVLGTELTPINGREERTPCYKOTLSFTGLTCIVSLVATGNVAVLMLGCRMRNA 60
Qy 76 VSIYIILNLVAADPLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 135
Db 61 VSIYIILNLVAADPLFLSGHIIICSPRLINIRHPISKILSPVMTFPYFGLSMLSAISTER 120
Qy 136 CUSIIMPIMWHCRPRRLSSVMCVLMLALSILSLIEMMCDPLFGSADSVWCETSDPIT 155
Db 121 CUSIIMPIMWHCRPRRLSSVMCVLMLALSILSLIEMMCDPLFGSADSVWCETSDPIT 180
Qy 196 IAMLVPLCVLCCSSSLVLRILGSRKMPRLRYTITLTVLVLGCLPFGIQMALFS 255

Db 181 IAMLVPLCVLCCSSSLVLRILGSRKMPRLRYTITLTVLVLGCLPFGIQMALFS 240
Qy 256 RIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQRALQDTPR 315
Db 241 RIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQNLKVLQRALQDTPR 300

RESULT 9

US-10-401-397A-2
; Sequence 2, Application US/10401397A
; Publication No. US20030212001A1
; GENERAL INFORMATION:
; APPLICANT: Perit, Kriehna G.
; APPLICANT: Moffett, Serge
; APPLICANT: Abbar, Daniel
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION AND TREATMENT OF ELEVATED
; FILE REFERENCE: 4518/1M674US1
; CURRENT APPLICATION NUMBER: US/10/401, 397A
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/367,513
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-397A-2

Query Match 82.2%; Score 277; DB 14; Length 322;

Best Local Similarity 100.0%; Pred. No. 3.6e-245;

Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 AVVLMGLGCRMRNAVSIYIILNLVAADPLFLSGHIIICSPRLINIRHPISKILSPVMTFP 120
Db 46 AVVLMGLGCRMRNAVSIYIILNLVAADPLFLSGHIIICSPRLINIRHPISKILSPVMTFP 105
Qy 121 YFGLSMLSAISTERCLSTIMPIMWHCRPRRLSSVMCVLMLALSILSLIEMMCDPLF 180
Db 106 YFGLSMLSAISTERCLSTIMPIMWHCRPRRLSSVMCVLMLALSILSLIEMMCDPLF 165
Qy 181 SGADSVWCETSDPITLTVLVLGCLPFGIQMALFSRIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQ 240
Db 166 SGADSVWCETSDPITLTVLVLGCLPFGIQMALFSRIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQ 225
Qy 241 LILGCLPFGIQMALFSRIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQ 300
Db 226 LILGCLPFGIQMALFSRIHDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRORONRQ 285
Qy 301 NLKVLQRALQDTPRVDGGMPLPOETLESGSRLEQ 337
Db 286 NLKVLQRALQDTPRVDGGMPLPOETLESGSRLEQ 322

RESULT 10

US-10-391-074-2
; Sequence 2, Application US/10391074
; Publication No. US20040038345A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael
; APPLICANT: Matlier, Frank
; TITLE OF INVENTION: No. US20040038345A1 Human Seven-Transmembrane Receptors
; FILE REFERENCE: 7705.0008-00-000
; CURRENT APPLICATION NUMBER: US/10/391, 074
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0.
; SEQ ID NO 2
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapien

US-10-391-074-2

Query Match 66.5%; Score 224; DB 15; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.3e-196;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 SPLRLINIRHPIISKILSPVMTFPYPIGLSMISAISTERCLSLMPIMWYHCRBPRYLSSVM 157
DB 83 SPLRLINIRHPIISKILSPVMTFPYPIGLSMISAISTERCLSLMPIMWYHCRBPRYLSSVM 142
QY 158 CVLLMALSLRSLIEMWPCDPLFGSGADSVWCETSPFITAMLVPLCVLCCSSVLVARI 217
DB 143 CVLLMALSLRSLIEMWPCDPLFGSGADSVWCETSPFITAMLVPLCVLCCSSVLVARI 202
QY 218 LCGSRKMPLTRLYVTITLTVLVEFLCGLPFGIOMLFSRIHDMKVLFCGHVLSIFLSA 277
DB 203 LCGSRKMPLTRLYVTITLTVLVEFLCGLPFGIOMLFSRIHDMKVLFCGHVLSIFLSA 262
QY 278 LNSSANPIIYFVGSFRQRONRQNLKVLQRLADTPEVDEGGG 321
DB 263 LNSSANPIIYFVGSFRQRONRQNLKVLQRLADTPEVDEGGG 306

RESULT 11

US-10-292-798-1274
; Sequence 1274, Application US/10292798
; Publication No. US20030235633A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABRATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1274
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-1274

Query Match 65.6%; Score 221; DB 14; Length 322;

Best Local Similarity 99.7%; Pred. No. 7.2e-194;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 MDSTIPVGTETPTINGREBETPCYKQTLSFTGLTCTIVSVALTGNAVYLMILGCMRRNA 75
DB 1 MDSTIPVGTETPTINGREBETPCYKQTLSFTGLTCTIVSVALTGNAVYLMILGCMRRNA 60
QY 76 VSIYILNLVADPLFLSGHIIICSPRLINIRHPIISKILSPVMTFPYPIGLSMISAISTER 135
DB 61 VSIYILNLVADPLFLSGHIIICSPRLINIRHPIISKILSPVMTFPYPIGLSMISAISTER 120
QY 136 CLSLIMPIMWYHCRBPRYLSSVMCVLLMALSLRSLIEMWPCDPLFGSGADSVWCETSDFIT 195
DB 121 CLSLIMPIMWYHCRBPRYLSSVMCVLLMALSLRSLIEMWPCDPLFGSGADSVWCETSDFIT 180
QY 196 IAMLVPLCVLCCSSVLVARIILCGSRKMPLTRLYVTITLTVLVEFLCGLPFGIOMALFS 255
DB 181 IAMLVPLCVLCCSSVLVARIILCGSRKMPLTRLYVTITLTVLVEFLCGLPFGIOMALFS 240
QY 256 RIHDMKVLFCGHVLSIFLSALNSSANPIIYFVGSFRQRONRQNLKVLQRLADTPE 315
DB 241 RIHDMKVLFCGHVLSIFLSALNSSANPIIYFVGSFRQRONRQNLKVLQRLADTPE 300
QY 316 VDEGGWLPQETLRLSGSRLRQ 337

DB 301 VDEGGWLPQETLRLSGSRLRQ 322

RESULT 12

US-10-072-012-530
; Sequence 530, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Bsha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Raetelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Groesse, William M.
; APPLICANT: Alebrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 530
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-530

Query Match 65.6%; Score 221; DB 15; Length 322;

Best Local Similarity 99.7%; Pred. No. 7.2e-194;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 MDSTIPVGTETPTINGREBETPCYKQTLSFTGLTCTIVSVALTGNAVYLMILGCMRRNA 75
DB 1 MDSTIPVGTETPTINGREBETPCYKQTLSFTGLTCTIVSVALTGNAVYLMILGCMRRNA 60

```
QY 76 VSIIYIINLVADPFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
DB 61 VSIIYIINLVADPFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 120
QY 136 CUSIIMPWYHCRPRYLSVWCVLMLALSLRLSIEMFCDPLFGADSVWCETSDPIT 195
DB 121 CUSIIMPWYHCRPRYLSVWCVLMLALSLRLSIEMFCDPLFGADSVWCETSDPIT 180
QY 196 IAMLVFLCVLGGSSVLVLRILICGSRKMPRLRYTYITLTVLVPFLCGLPFGIOWALFS 255
DB 181 IAMLVFLCVLGGSSVLVLRILICGSRKMPRLRYTYITLTVLVPFLCGLPFGIOWALFS 240
QY 256 RIHLDMKVLFCVHLVSIPLSALNSSANPIYFVGSFRORONRQNLKVLQALQDTPR 315
DB 241 RIHLDMKVLFCVHLVSIPLSALNSSANPIYFVGSFRORONRQNLKVLQALQDTPR 300
QY 316 VDEGGMLPQETTELSSGRLEQ 337
DB 301 VDEGGMLPQETTELSSGRLEQ 322

RESULT 13
US-10-072-012-535
; Sequence 535, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchemnev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zehusen, Bryan
; APPLICANT: Patunajan, Meera
; APPLICANT: Shimkete, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Beha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimyr Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosee, William M.
; APPLICANT: Alsodrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine B.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 535
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-535

Query Match 65.7%; Score 221; DB 15; Length 322;
Best Local Similarity 99.7%; Pred. No. 7.2e-194;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 MDSTIPLVLTETLPINGREETPCYKQTLSTFTGLTCIVSIVALTGNVAVMLGCRNRNA 75
DB 1 MDSTIPLVLTETLPINGREETPCYKQTLSTFTGLTCIVSIVALTGNVAVMLGCRNRNA 60
QY 76 VSIIYIINLVADPFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
DB 61 VSIIYIINLVADPFLSGHIIICSPRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 120
QY 136 CUSIIMPWYHCRPRYLSVWCVLMLALSLRLSIEMFCDPLFGADSVWCETSDPIT 195
DB 121 CUSIIMPWYHCRPRYLSVWCVLMLALSLRLSIEMFCDPLFGADSVWCETSDPIT 180
QY 196 IAMLVFLCVLGGSSVLVLRILICGSRKMPRLRYTYITLTVLVPFLCGLPFGIOWALFS 255
DB 181 IAMLVFLCVLGGSSVLVLRILICGSRKMPRLRYTYITLTVLVPFLCGLPFGIOWALFS 240
QY 256 RIHLDMKVLFCVHLVSIPLSALNSSANPIYFVGSFRORONRQNLKVLQALQDTPR 315
DB 241 RIHLDMKVLFCVHLVSIPLSALNSSANPIYFVGSFRORONRQNLKVLQALQDTPR 300
QY 316 VDEGGMLPQETTELSSGRLEQ 337
DB 301 VDEGGMLPQETTELSSGRLEQ 322

RESULT 14
US-10-237-467-10
; Sequence 10, Application US/10237467
; Publication No. US20030186324A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Jiayu
; APPLICANT: Gray, Nathanael S.
; APPLICANT: Caldwell, Jeremy C.
; APPLICANT: Schultz, Peter G.
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Sensory Neuron Receptors
; FILE REFERENCE: 021288-001300US
; CURRENT APPLICATION NUMBER: US/10/237,467
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/317,879
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 10
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
; OTHER INFORMATION: 7 (DRG7) (NT09307)
US-10-237-467-10

Query Match 53.7%; Score 181; DB 14; Length 302;
Best Local Similarity 99.6%; Pred. No. 3e-157;
Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 ALTGNAVITMLGCRNRNAVSIYIINLVADPFLSGHIIICSPRLINIRHPISKILSP 115
DB 21 ALTGNAVITMLGCRNRNAVSIYIINLVADPFLSGHIIICSPRLINIRHPISKILSP 80
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OM protein - protein search, using sw model

Run on: October 27, 2004, 08:43:20 ; Search time 39 Seconds

(without alignments)
831.412 Million cell updates/sec

Title: US-09-867-570-2

Perfect score: 337

Sequence: 1 MESKSSWVIRLIGFLSMDSTI.....EGGGWLPGETLRLSGRLAQ 337

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched:

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: PIR.79:.*
2: PIR1:.*
3: PIR2:.*
4: PIR3:.*
5: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	4.2	378	2	A39485 transforming prote
2	10	3.0	435	2	A44308 Antho-Rfamide prec
3	8	2.4	111	2	S16099 viacotoxin - Europ
4	8	2.4	141	2	C81055 hypothetical prote
5	8	2.4	141	2	B81822 hypothetical prote
6	8	2.4	215	2	JS0037 somatotropin precu
7	8	2.4	215	2	IS1188 somatotropin - bul
8	8	2.4	230	2	I48685 mast cell proteina
9	8	2.4	276	2	A38654 mast cell proteina
10	8	2.4	411	2	T39481 hypothetical prote
11	8	2.4	429	2	F82679 conserved hypochet
12	8	2.4	455	2	G70089 hypothetical prote
13	8	2.4	541	2	AH2909 hypothetical prote
14	8	2.4	541	2	F97684 thiamin transport
15	8	2.4	984	2	T50309 hypothetical WD-re
16	7	2.1	49	1	LBHCB light-harvesting p
17	7	2.1	50	1	LBHCB light-harvesting p
18	7	2.1	71	2	B45874 ig alpha-1 chain C
19	7	2.1	125	2	C72579 ig alpha-2 chain C
20	7	2.1	160	2	AB1185 B. subtilis Yds p
21	7	2.1	163	2	H75203 probable biotin sy
22	7	2.1	174	2	B75114 probable NADH dehy
23	7	2.1	179	2	B70757 hypothetical prote
24	7	2.1	181	2	F69138 hypothetical prote
25	7	2.1	186	2	F90150 conserved hypochet
26	7	2.1	199	2	JU0052 puromycin N-acetyl
27	7	2.1	209	2	C70424 hypothetical prote
28	7	2.1	213	2	T27841 hypothetical prote
29	7	2.1	213	2	T27841

30	7	2.1	256	2	A11119 transcription regu
31	7	2.1	256	2	AD1480 transcription regu
32	7	2.1	260	2	AD1481 hypothetical prote
33	7	2.1	263	2	S48498 oxidoreductase hom
34	7	2.1	269	2	C71255 conserved hypochet
35	7	2.1	270	2	S16579 chitinase (EC 3.2.
36	7	2.1	276	2	S35270 DNA-damage repair
37	7	2.1	284	2	AH0415 probable membrane-
38	7	2.1	298	2	F82356 transcription acti
39	7	2.1	300	2	T26245 hypothetical prote
40	7	2.1	301	2	F86440 unknown protein [i
41	7	2.1	303	2	B96909 probable permease
42	7	2.1	313	2	AB2203 hypothetical prote
43	7	2.1	315	2	T49982 hypothetical prote
44	7	2.1	322	2	T24525 hypothetical prote
45	7	2.1	324	1	TVRTAS transforming prote

ALIGNMENTS

RESULT 1
A39485
transforming protein (mrg) - human
C/Species: Homo sapiens (man)
C/Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C/Accession: A39485
R/Monot, C., Weber, V., Stinake, J., Bihoreau, C., Teutsch, B., Corvol, P., Clauser, J.
Mol. Endocrinol. 5, 1477-1487, 1991
A/Title: Cloning and functional characterization of a novel mas-related gene, modulating
A/Reference number: A39485, MUID:9210997; PMID:1723144
A/Accession: A39485
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-378 <MON>
A/Species: Anthopleura elegantissima
C/Species: Anthopleura elegantissima
C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A44308
J. Biol. Chem. 267, 22534-22541, 1992
R/Schultz, C., Darmer, D., Diekhoff, D., Grimmelikhuijzen, C.J.
A/Title: Identification of a novel type of processing sites in the precursor for the sea
A/Reference number: A44308; MUID:93054550; PMID:1429603
A/Accession: A44308
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-435 <SCH>
A/Cross-references: UNIPROT:P10419; GB:M98269; NID:G155702; PIDN:AAA2738.1; PID:G155703
A/Note: sequence extracted from NCBI backbone (NCBIN:117102, NCBI:P.117104)
C/Keywords: neuropeptide

Query Match 4.2%; Score 14; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 279 NSSANPIYFVGS 292
Db 306 NSSANPIYFVGS 319

RESULT 2

A44308
Antho-Rfamide precursor - sea anemone (Anthopleura elegantissima)
C/Species: Anthopleura elegantissima
C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A44308
J. Biol. Chem. 267, 22534-22541, 1992
R/Schultz, C., Darmer, D., Diekhoff, D., Grimmelikhuijzen, C.J.
A/Title: Identification of a novel type of processing sites in the precursor for the sea
A/Reference number: A44308; MUID:93054550; PMID:1429603
A/Accession: A44308
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-435 <SCH>
A/Cross-references: UNIPROT:P10419; GB:M98269; NID:G155702; PIDN:AAA2738.1; PID:G155703
A/Note: sequence extracted from NCBI backbone (NCBIN:117102, NCBI:P.117104)
C/Keywords: neuropeptide

Query Match 3.0%; Score 10; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 YVITLLTVLV 239
Db 6 YVITLLTVLV 15

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RESULT 3
S16099
A:Species: Viacetum album (European mistletoe)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S16099
R:Schrader, G.; Apel, K.
Eur. J. Biochem. 198, 549-553, 1991
A:Title: Isolation and characterization of cDNAs encoding visco toxins of mistletoe (Visc
A:Reference number: S16099; MUID:91266334; PMID:1710983
A:Accession: S16099
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <EUR>
C:Superfamily: visco toxin

Query Match      2.4%; Score 8; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      208 GSSLVTLV 215
Db      6 GSSLVTLV 13

RESULT 4
C81055
A:Species: Neisseria meningitidis (strain MCS8 serogroup
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81055
R:Tettein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.R.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: C81055
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <TET>
A:Cross-references: UNIPROT:Q9JY98; GB:AE002518; GB:AE002098; NID:G7226928; PIDN:AAF4202
A:Experimental source: serogroup B, strain MCS8
C:Genetics:
A:Gene: NMB1681

Query Match      2.4%; Score 8; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      146 HCRPRRYL 153
Db      71 HCRPRRYL 78

RESULT 5
B81822
A:Species: Neisseria meningitidis (strain Z2491 serogroup
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: B81822
R:Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: B81822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <PAR>

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A:Cross-references: UNIPROT:Q9JY80; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CA8516C
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1940

Query Match      2.4%; Score 8; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      146 HCRPRRYL 153
Db      71 HCRPRRYL 78

RESULT 6
JS0037
A:Species: Rana catesbeiana (bullfrog)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JS0037; PS0310
R:Pan, F.M.; Chang, W.C.
Biochim. Biophys. Acta 950, 238-242, 1988
A:Title: Cloning and sequencing of bullfrog growth hormone complementary DNA.
A:Reference number: JS0037; MUID:88252154; PMID:3260110
A:Accession: JS0037
A:Molecule type: mRNA
A:Residues: 1-215 <PAN>
A:Cross-references: UNIPROT:P10813; GB:X12520; NID:G64259; PIDN:CAA31038.1; PID:G64260
A:Accession: PS0310
A:Molecule type: protein
A:Residues: 26-55 <PAZ>
C:Comment: This protein is synthesized and secreted by the anterior pituitary gland and
C:Superfamily: prolactin
C:Keywords: growth factor; hormone
P1-25/Domain: signal sequence #status predicted <SIG>
P126-215/Product: somatotropin #status experimental <MAT>

Query Match      2.4%; Score 8; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      208 GSSLVTLV 215
Db      6 GSSLVTLV 13

RESULT 7
IS1188
A:Species: Rana catesbeiana (bullfrog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: IS1188
R:Takahashi, N.; Kikuyama, S.; Gen, K.; Maruyama, O.; Kato, Y.
J. Mol. Endocrinol. 9, 283-289, 1992
A:Title: Cloning of a bullfrog growth hormone cDNA: expression of growth hormone mRNA in
A:Reference number: IS1188; MUID:93119453; PMID:1476615
A:Accession: IS1188
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-215 <TAK>
A:Cross-references: UNIPROT:P10813; GB:SS2027; NID:G262921; PIDN:AA824792.1; PID:G262922
C:Superfamily: prolactin

Query Match      2.4%; Score 8; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      208 GSSLVTLV 215
Db      6 GSSLVTLV 13

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RESULT 8
I48685
mact cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I48685; S43172
R/Huang, R.; Hellman, L.
Immunogenetics 40, 397-414, 1994
A/Title: Genes for mact-cell serine protease and their molecular evolution.
A/Reference number: I48684; MUID:95048582; PMID:7959952
A/Accession: I48685
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-230 <RES>
A/Cross-references: UNIPROT:P21845; EMBL:X78542; NID:9468809; PIDN:CAA55288.1; PID:94688
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; serine proteinase
F/22-230/Domain: trypsin homology #status atypical <TRY>

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 230;
Pred. No. 5.5; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 LLMALSL 167
Db 8 LLMALSL 15

RESULT 9
A38654
mact cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: A38654; B38654; D35646; I59478
R/Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.B.
J. Biol. Chem. 266, 3847-3853, 1991
A/Title: Cloning of the cDNA and gene of mouse mact cell proteinase-6. Transcription by p
A/Reference number: A38654; MUID:91139682; PMID:1995638
A/Accession: A38654
A/Molecule type: DNA
A/Residues: 1-276 <REV>
A/Cross-references: UNIPROT:P21845; GB:M57625; NID:9200506; PIDN:AAA3987.1; PID:9200507
A/Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37 a
s Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
A/Accession: B38654
A/Molecule type: mRNA
A/Residues: 1-276 <RES>
A/Cross-references: GB:M57626; NID:9200508; PIDN:AAA3988.1; PID:9200509
R/Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A/Title: Different mouse mact cell populations express various combinations of at least
A/Reference number: A35646; MUID:90222202; PMID:2326280
A/Accession: D35646
A/Molecule type: protein
A/Residues: 32-54 <RES>
R/Huang, R.; Abrik, M.; Gohl, A.E.; Nilsson, G.; Aveskog, M.; Larsson, L.G.; Nilsson,
Scand. J. Immunol. 38, 359-367, 1993
A/Title: Expression of a mact cell trypsin in the human monocytic cell lines U-937 and
A/Reference number: I59478; MUID:94023807; PMID:8210998
A/Accession: I59478
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-276 <RES>
A/Cross-references: GB:U31853; NID:9473480; PIDN:AAA39725.1; PID:9473481
C/Genetics:
A/Gene: MMCP-6
A/Intons: 24/1; 79/2; 168/1; 222/3
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; serine proteinase; zymogen
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-31/Domain: activation peptide #status predicted <ACT>
F/32-276/Product: mact cell proteinase 6 #status experimental <MAT>

F/32-268/Domain: trypsin homology <TRY>
F/75,122,225/Active site: His, Asp, Ser #status predicted

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 276;
Pred. No. 6.4; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 LLMALSL 167
Db 8 LLMALSL 15

RESULT 10
T39481
hypothetical protein SPBC15D4.05 - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T39481
R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gallard, C.
submitted to the EMBL Data Library, August 1997
A/Reference number: Z21858
A/Accession: T39481
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-411 <LYN>
A/Cross-references: UNIPROT:O74310; EMBL:AL031349; PIDN:CAA20480.1; GSPDB:GN00067; SPDB:
A/Experimental source: strain 972h-; cosmid c15D4
C/Genetics:
A/Gene: SPDB:SPBC15D4.05
A/Map position: 2

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 411;
Pred. No. 9; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 SLRSLR 172
Db 76 SLRSLR 83

RESULT 11
F82679
conserved hypothetical protein XFI453 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: F82679
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: F82679
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-429 <SIM>
A/Cross-references: UNIPROT:Q9PDC6; GB:AE003975; GB:AE003849; NID:99106468; PIDN:AF8426;
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reineck, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; Al
Birtone, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carier, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Frana, S.C.; Franco, M.C.; Frome
J.D.; Junqueira, M.L.; Kemper, E.L.; Kiteajima, U.P.; Krieger, J.E.; Kurame, E.B.; Laifre
chado, W.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B
A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miteca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XFI453

C;Superfamily: Haemophilus influenzae conserved hypothetical protein HII590

Query Match 2.4%; Score 8; DB 2; Length 429;

Best Local Similarity 100.0%; Pred. No. 9.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 LQALQDT 313

DB 155 LQALQDT 162

RESULT 12

G70089 hypothetical protein yycH - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G70089

R;Kunitz, F.; Ogatawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emerson, P.T.; Ehtian, K.D.; Ertlington, J.; Fabret, C.; Ferrati, B.; Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Galliech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpere, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunori, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G70089

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-455 <KUN>

A;Cross-references: UNIPROT:Q45613; GB:Z99124; GB:AL009126; NID:G2636442; PIDN:CAB16076.

A;Experimental source: strain 168

C;Genetics:

A;Gene: yycH

C;Superfamily: Bacillus subtilis hypothetical protein yycH

Query Match 2.4%; Score 8; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 TILTLVLY 239

DB 8 TILTLVLY 15

RESULT 13

AH2909 hypothetical protein thip [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AH2909

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, B.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AH2909

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-541 <KUR>

A;Cross-references: UNIPROT:Q8UBV5; GB:AE008688; PIDN:AL45694.1; PID:917741221; GSPDB:C

A;Gene: thip

A;Map position: circular chromosome

Query Match 2.4%; Score 8; DB 2; Length 541;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GSSLVLY 215

DB 378 GSSLVLY 385

RESULT 14

F97684 thiamin transport system permease protein thip [imported] - Agrobacterium tumefaciens (st

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C;Accession: F97684

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: F97684

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: UNIPROT:Q8UBV5; GB:AE007869; PIDN:AK88431.1; PID:915157926; GSPDB:GT

C;Genetics:

A;Gene: AGR_C_4917

A;Map position: circular chromosome

Query Match 2.4%; Score 8; DB 2; Length 541;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GSSLVLY 215

DB 378 GSSLVLY 385

RESULT 15

T50309 hypothetical WD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C;Accession: T50309

R;Brown, S.; Harris, D.; McDougall, R.C.; Rejandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, November 1999

A;Reference number: Z25060

A;Accession: T50309

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-584 <BRO>

A;Cross-references: UNIPROT:Q9USZ0; EMBL:AL133303; PIDN:CA862092.1; GSPDB:GN00067; SPDB:6

A;Experimental source: strain 972h(-); cosmid c1306

C;Genetics:

A;Gene: SPBC4.08; SPDB:SPBC1306.02

A;Map position: 2

A;Intons: 349/2; 565/3

Query Match 2.4%; Score 8; DB 2; Length 984;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 SSANPIY 287

DB 290 SSANPIY 297

Search completed: October 27, 2004, 08:53:08

Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2004, 08:35:09 : Search time 196 Seconds
(without alignments)
989.292 Million cell updates/sec

Title: US-09-867-570-2

Perfect score: 337

Sequence: 1 MSKSKSWVRLGFLSMDSTI.....EGSGWLPGFTLBSGRLAQ 337

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: uniprot_02:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	322	95.5	322	1	MRG3_HUMAN
2	224	66.5	322	1	AH67292
3	86	25.5	322	1	SNS2_HUMAN
4	50	14.8	322	1	MRG1_HUMAN
5	44	13.1	322	1	SNS3_HUMAN
6	41	12.2	322	1	MRG4_HUMAN
7	41	12.2	322	1	SNS5_HUMAN
8	20	5.9	330	2	MRG2_HUMAN
9	20	5.9	330	2	AH63450
10	15	4.5	302	1	MG43_MOUSE
11	15	4.5	304	1	MG41_MOUSE
12	15	4.5	304	1	MG42_MOUSE
13	15	4.5	305	1	MG47_MOUSE
14	15	4.5	305	1	MG48_MOUSE
15	15	4.5	313	1	MG44_MOUSE
16	15	4.5	313	1	MG45_MOUSE
17	14	4.2	378	1	MRG_HUMAN
18	14	4.2	378	1	AH69345
19	13	3.9	301	1	MG46_MOUSE
20	13	3.9	305	1	MG42_MOUSE
21	13	3.9	331	2	AH64040
22	11	3.3	294	2	Q7TN48
23	11	3.3	304	1	MG45_MOUSE
24	11	3.3	323	1	SNS1_RAT
25	11	3.3	323	2	Q7TN42
26	11	3.3	323	2	Q7TN45
27	10	3.0	312	2	Q91ZC1
28	10	3.0	322	2	Q8C1P3
29	10	3.0	429	1	FMR2_ANTHEL
30	10	3.0	435	1	FMR1_ANTHEL
31	9	2.7	321	2	Q7TN38

32	9	2.7	353	2	Q7TN44	Q7tn44 ratu
33	9	2.7	399	2	Q75XU5	Q75xu5 gallu
34	9	2.7	399	2	BAC87782	BAC87782 gallu
35	9	2.7	430	1	NPPL_HUMAN	NPPL_HUMAN
36	8	2.4	111	1	THN3_VISAL	THN3_VISAL
37	8	2.4	116	2	Q9HBE6	Q9HBE6
38	8	2.4	116	2	Q96H14	Q96H14
39	8	2.4	141	2	Q9J780	Q9J780
40	8	2.4	141	2	Q9JY98	Q9JY98
41	8	2.4	156	2	Q711N2	Q711N2
42	8	2.4	156	2	CAC6130	CAC6130
43	8	2.4	164	2	Q82858	Q82858
44	8	2.4	215	1	SOMA_RANCA	SOMA_RANCA
45	8	2.4	215	2	Q7ZU47	Q7ZU47

ALIGNMENTS

RESULT 1
MRG3_HUMAN STANDARD; PRT; 322 AA.
ID MRG3_HUMAN
AC Q96L80; Q8TDE1;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Mas-related G-protein coupled receptor member X3 (Sensory neuron-specific G-protein coupled receptor 1).
GN Name=MRG3; Synonyms=SNSR1;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=11853733; PubMed=11551509;
RA Dong X., Han S.-K., Zyika M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of nociceptive sensory neurons."
RL Cell 106:619-632(2001).
RN [2]
RP SEQUENCE FROM N.A., VARIANT ASN-169, AND TISSUE SPECIFICITY.
RX MEDLINE=21853733; PubMed=1150634; DOI=10.1038/nr15;
RA Lembo P.M.C., Grazzini B., Groblewski T., O'Donnell D., Roy M.-O., Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M., Gosselin M., Fortin Y., Barville D., Shen S., Stroem P., Payza K., Dray A., Walker P., Ahmad S.;
RT "Proenkephalin A gene products activate a new family of sensory neuron-specific GPCRs."
RL Nat. Neurosci. 5:201-209(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh P., Datchenko L., Matulis K., Farmer A.A., Rubin G.M., Hong L., Stamps M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Udell T.B., Tohyuki S., Carninci P., Prange C., Raba S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallian D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 CC nociceptive neurons. May regulate nociceptor function and/or
 CC development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 CC root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Mas subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AY042215; AAK91806.1; -
 CC EMBL: AF474987; AAL86878.2; -
 CC EMBL: BC067292; AAB67292.1; -
 CC MIM: 607229; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm1.1; -
 CC PRINTS: PR00237; GPCR_RHODOPSIN.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 CC PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Polymorphic; Transmembrane.
 CC DOMAIN 1 31 Extracellular (Potential).
 CC TRANSSEM 32 52 1 (Potential).
 CC TRANSSEM 53 60 Cytoplasmic (Potential).
 CC TRANSSEM 61 81 2 (Potential).
 CC TRANSSEM 82 96 Extracellular (Potential).
 CC TRANSSEM 97 117 3 (Potential).
 CC TRANSSEM 118 140 Cytoplasmic (Potential).
 CC TRANSSEM 141 161 4 (Potential).
 CC TRANSSEM 162 177 Extracellular (Potential).
 CC TRANSSEM 178 198 5 (Potential).
 CC TRANSSEM 199 213 Cytoplasmic (Potential).
 CC TRANSSEM 214 234 6 (Potential).
 CC TRANSSEM 235 254 Extracellular (Potential).
 CC TRANSSEM 255 275 7 (Potential).
 CC TRANSSEM 276 322 Cytoplasmic (Potential).
 CC VARIANT 169 169 D -> N (in dbSNP:4274188).
 CC CONFLICT 3 3 S -> P (in Ref. 2).
 CC CONFLICT 82 82 C -> R (in Ref. 3).
 CC CONFLICT 307 307 W -> Q (in Ref. 3).
 CC CONFLICT 319 319 R -> K (in Ref. 2).
 CC SEQUENCE 322 AA; 36484 MW; 2531BBF0CB4EB74 CRC64;
 SQ
 Query Match 95.5%; Score 322; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 3e-311;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 RHLDWKVLFCHVHVSIFLSALNSSANPITVFVGSFRORONKLVLRALQDTPPE 300
 QY 316 VDEGGWLPORTELSSRLQ 337
 Db 301 VDEGGWLPORTELSSRLQ 322
 RESULT 2
 AAH67292 PRELIMINARY; PRT; 322 AA.
 ID AAH67292; (Created)
 AC 25-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 25-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 25-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE G-protein-coupled receptor MRGX3.
 GN MRGX3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cairncup P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton K., Kettlemen M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalske U., Smallos D.B., Schnerch A., Schein J.B.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RA and mouse cDNA sequences";
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC067292; AAH67292.1; -
 KW Receptor.
 SQ SEQUENCE 322 AA; 36479 MW; B91DC082B6D95DA8 CRC64;
 Query Match 66.5%; Score 224; DB 2; Length 322;
 Best Local Similarity 100.0%; Pred. No. 9e-214;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 SNS2_HUMAN STANDARD; PRT; 322 AA.
 ID SNS2_HUMAN
 AC O8TDE0;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sensory neuron-specific G-protein coupled receptor 2.
 GN Name=SNR2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nr815;
 RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
 RA Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
 RA Dray A., Walker P., Ahmad S.;
 RT "Proenkephalin A gene products activate a new family of sensory
 neuron-specific GPCRs.";
 RL Nat. Neurosci. 5:201-209(2002).
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 nociceptive neurons. May regulate nociceptor function and/or
 development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Was subfamily.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF474988; AAL86879.2; -;
 DR InterPro: IPR000276; GPCR_Rhodopn.
 DR Pfam: PF00001; 7tm_1, 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_F2_1; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 32
 FT TRANSMEM 33 53
 FT DOMAIN 54 60
 FT TRANSMEM 61 81
 FT DOMAIN 82 96
 FT TRANSMEM 97 117
 FT DOMAIN 118 140
 FT TRANSMEM 141 161
 FT DOMAIN 162 177
 FT TRANSMEM 178 198
 FT DOMAIN 199 213
 FT TRANSMEM 214 234
 FT DOMAIN 235 254
 FT TRANSMEM 255 275
 FT DOMAIN 276 322
 FT CARBOHYD 89
 SEQUENCE 322 AA; 36594 MW; D8C24308B3B4611B CRC64;
 Query Match 25.5%; Score 86; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 1.7e-76;
 Matches 86; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

Db 189 VVLGSSLVLVRLTLCGRMKPLRLVLTLLVFLVLCGLPFGIOMALFSLRHLDMKV 248
 Qy 264 LFCVHLVSLVPLSALNSANPIIYFF 289
 Db 249 LFCVHLVSLVPLSALNSANPIIYFF 274
 RESULT 4
 MRG1_HUMAN STANDARD; PRT; 322 AA.
 ID MRG1_HUMAN
 AC Q96LB2; Q8TDB8;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Mas-related G-protein coupled receptor member X1 (Sensory neuron-
 specific G-protein coupled receptor 4).
 GN Name=MRGX1; Synonym=SNR4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=21435808; PubMed=11551509;
 RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
 RT "A diverse family of GPCRs expressed in specific subsets of
 nociceptive sensory neurons.";
 RL Cell 106:619-632(2001).
 RN [2]
 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nr815;
 RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
 RA Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
 RA Dray A., Walker P., Ahmad S.;
 RT "Proenkephalin A gene products activate a new family of sensory
 neuron-specific GPCRs.";
 RL Nat. Neurosci. 5:201-209(2002).
 RN [3]
 SEQUENCE FROM N.A.
 RX MEDLINE=22040266; PubMed=12044878;
 RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
 RT "Identification of G protein-coupled receptor genes from the human
 genome sequence.";
 RL F585 Lett. 520:97-101(2002).
 RN [4]
 SEQUENCE FROM N.A.
 RP Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tautani S., Aburatani H., Asai K., Akiyama Y.;
 RT "genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 nociceptive neurons. May regulate nociceptor function and/or
 development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins including BAW2 (bovine adrenal
 medulla peptide 22) and BAM (8-22). BAW2 is the most potent
 compound and evoked a large and dose-dependent release of
 intracellular calcium in stably transfected cells. G(alpha)q
 proteins are involved in the calcium-signaling pathway.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Was subfamily.
 CC -----
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CC or send an email to license@lsb-sib.ch).

CC -----

DR EMBL: AY042213; AAK91804.1; -

DR EMBL: AF474990; AAL86881.1; -

DR EMBL: AB083628; BAB89341.1; -

DR EMBL: AB065846; BAC06064.1; -

DR MIM: 607227; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHDOPSN.

DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; 1.

DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.

DR G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.

KW DOMAIN 1 31

FT TRANSSEM 32 52

FT DOMAIN 53 67

FT TRANSSEM 68 88

FT DOMAIN 89 96

FT TRANSSEM 97 117

FT DOMAIN 118 144

FT TRANSSEM 145 165

FT DOMAIN 166 177

FT TRANSSEM 178 198

FT DOMAIN 199 221

FT TRANSSEM 222 242

FT DOMAIN 243 254

FT TRANSSEM 255 275

FT DOMAIN 276 322

FT CARBOHYD 16 16

FT VARIANT 36 36

FT N-linked (GlcNAc...) (potential).

FT I -> V (in dbSNP:11024885).

FT /FTID=VAR_019432.

FT I -> V (in Ref. 2).

FT CONFLICT 5 5

FT SQ SEQUENCE 322 AA; 36250 MW; C7F3A9F4418E8AD1 CRC64;

Query Match 14.8%; Score 50; DB 1; Length 322;

Best Local Similarity 100.0%; Pred. No. 1.1e-40; Indels 0; Gaps 0;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 VLFCVHLVSLFSLNLSNANPIYFVFGSFQRQRNQLKVLORALD 312

DB 248 VLFCVHLVSLFSLNLSNANPIYFVFGSFQRQRNQLKVLORALD 297

RESULT 5

SNS3_HUMAN STANDARD; PRT; 322 AA.

AC OBTDD9;

DT 01-OCT-2004 (Rel. 45, Created)

DT 01-OCT-2004 (Rel. 45, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Sensory neuron-specific G-protein coupled receptor 3.

GN Name=SNSR3;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RX MEDLINE=2185733; PubMed=11850634; DOI=10.1038/nm815;

RA Lembo P.M.C., Grazzini B., Groblewski T., O'Donnell D., Roy M.O., Zhang J., Hoffer C., Cao J., Schmidt R., Pelletier M., Labarre M., Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K., Dray A., Walker P., Ahmad S.,

RA "Proenkephalin A gene products activate a new family of sensory neuron-specific GPCRs";

RT neuron-specific GPCRs";

RL Nat. Neurosci. 5:201-209(2002).

CC - FUNCTION: Orphan receptor. Probably involved in the function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. CC potentially activated by enkephalins including BAW22 (bovine adrenal medulla peptide 22) and BAM (8-22). BAW22 is the most potent CC compound and evoked a large and dose-dependent release of intracellular calcium in stably transfected cells. (Alpha)q

CC proteins are involved in the calcium-signaling pathway.

CC - SUBCELLULAR LOCATION: Integral membrane protein.

CC - TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeminal sensory neurons.

CC - SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Mas subfamily.

CC -----

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CC -----

DR EMBL: AF474989; AAL86880.2; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHDOPSN.

DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; 1.

DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.

DR G-protein coupled receptor; Glycoprotein; Transmembrane.

KW DOMAIN 1 31

FT TRANSSEM 32 52

FT DOMAIN 53 67

FT TRANSSEM 68 88

FT DOMAIN 89 96

FT TRANSSEM 97 117

FT DOMAIN 118 144

FT TRANSSEM 145 165

FT DOMAIN 166 177

FT TRANSSEM 178 198

FT DOMAIN 199 221

FT TRANSSEM 222 242

FT DOMAIN 243 254

FT TRANSSEM 255 275

FT DOMAIN 276 322

FT CARBOHYD 16 16

FT N-linked (GlcNAc...) (potential).

FT I -> V (in dbSNP:11024885).

FT /FTID=VAR_019432.

FT I -> V (in Ref. 2).

FT CONFLICT 5 5

FT SQ SEQUENCE 322 AA; 36287 MW; 4C43B3B52DCBFP5 CRC64;

Query Match 13.1%; Score 44; DB 1; Length 322;

Best Local Similarity 100.0%; Pred. No. 1e-34;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 RORNRNQLKVLORALDPEVDEGGWLPQETLEISGSRLRQ 337

DB 279 RORNRNQLKVLORALDPEVDEGGWLPQETLEISGSRLRQ 322

RESULT 6

MKG4_HUMAN STANDARD; PRT; 322 AA.

AC O96LA9; OBTDD6;

DT 01-OCT-2004 (Rel. 45, Created)

DT 01-OCT-2004 (Rel. 45, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Mas-related G-protein coupled receptor member X4 (Sensory neuron-specific G-protein coupled receptor 6).

GN Name=MKG4; Synonyms=SNSR6;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21435808; PubMed=11551509;

RA Dong X., Han S.-K., Zylika M.V., Simon M.I., Anderson D.J., RT "A diverse family of GPCRs expressed in specific subsets of nociceptive sensory neurons";

RL Cell 106:619-632(2001).

RN [2]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RX MEDLINE=2185733; PubMed=11850634; DOI=10.1038/nm815;

RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
 RA Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
 RA "Proenkephalin A gene products activate a new family of sensory
 RT neuron-specific GPCRs.",
 RL Nat. Neurosci. 5:201-209(2002).
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 CC nociceptive neurons. May regulate nociceptor function and/or
 CC development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 CC root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Was subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AY042216; AAK91807.1; -
 DR EMBL: AF474992; AAL86883.1; -
 DR MTM: 607230; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
 FT DOMAIN 1 31
 FT TRANSSEM 32 52
 FT TRANSSEM 53 60
 FT TRANSSEM 61 81
 FT DOMAIN 82 96
 FT TRANSSEM 97 117
 FT DOMAIN 118 137
 FT TRANSSEM 138 158
 FT TRANSSEM 159 177
 FT TRANSSEM 178 198
 FT DOMAIN 199 218
 FT TRANSSEM 219 239
 FT DOMAIN 240 254
 FT TRANSSEM 255 275
 FT DOMAIN 276 322
 FT CARBOHYD 25 25
 FT CARBOHYD 89 89
 FT VARIANT 8 8
 FT VARIANT 25 25
 FT VARIANT 54 54
 FT VARIANT 83 83
 FT CONFLICT 182 182
 FT CONFLICT 319 319
 FT SEQUENCE 322 AA; 36434 MW; 7CA676F8BD30A31 CRC64;
 Query Match 12.2%; Score 41; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 9,6e-32;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SNSS HUMAN
 ID SNSS HUMAN STANDARD; PRT; 322 AA.
 AC OR07D7;
 DT 01-OCT-2004 (Rel. 45, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sensory neuron-specific G-protein coupled receptor 5.
 GN Name=SNRS5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RX MEDLINE=21853733; PubMed=11850634; DOI=10.1038/an815;
 RA Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
 RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
 RA Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,
 RA Dray A., Walker P., Ahmad S.,
 RT "Proenkephalin A gene products activate a new family of sensory
 RT neuron-specific GPCRs.",
 RL Nat. Neurosci. 5:201-209(2002).
 CC -1- FUNCTION: Orphan receptor. Probably involved in the function of
 CC nociceptive neurons. May regulate nociceptor function and/or
 CC development, including the sensation or modulation of pain.
 CC Potentially activated by enkephalins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal
 CC root and trigeminal sensory neurons.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Was subfamily.
 CC -----
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 CC -----
 DR EMBL: AF474991; AAL86882.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 31
 FT TRANSSEM 32 52
 FT TRANSSEM 53 60
 FT TRANSSEM 61 81
 FT DOMAIN 82 96
 FT TRANSSEM 97 117
 FT DOMAIN 118 137
 FT TRANSSEM 138 158
 FT TRANSSEM 159 177
 FT TRANSSEM 178 198
 FT DOMAIN 199 218
 FT TRANSSEM 219 239
 FT DOMAIN 240 254
 FT TRANSSEM 255 275
 FT DOMAIN 276 322
 FT CARBOHYD 89 89
 FT SEQUENCE 322 AA; 36423 MW; 3D6F8B5DDFD90 CRC64;
 Query Match 12.2%; Score 41; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 9,6e-32;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
MRG2 HUMAN STANDARD; PRT; 330 AA.
ID MRG2 HUMAN STANDARD; PRT; 330 AA.
AC 0961B1;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Mas-related G-protein coupled receptor member X2.
Name=MRGX2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylika M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of
RT nociceptive sensory neurons."
RL Cell 106:619-632(2001).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22040266; PubMed=12044878;
RA Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence."
RL FEBS Lett. 520:97-101(2002).
[3]
RN
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arica M., Putani K., Matsumoto S.,
RA Tsubumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[4]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN
RP TISSUE SPECIFICITY, AND POSSIBLE FUNCTION.
RX PubMed=12915402; DOI=10.1074/jbc.M302456200;
RA Robas N., Mead E., Fiddock M.;
RT "MRGX2 is a high potency cortistatin receptor expressed in dorsal root
RT ganglion."
RL J. Biol. Chem. 278:44400-44404(2003).
[6]
RN
RP FUNCTION: Orphan receptor. Probably involved in the function of
CC nociceptive neurons. May regulate nociceptive function and/or
CC development, including the sensation or modulation of pain.
CC Cortistatin-14 seems to be a high potency ligand at this receptor.
CC Cortistatin has several biological functions including roles in
CC sleep regulation, locomotor activity, and cortical function. In
CC receptor-expressing cells, cortistatin-stimulated increases in

CC intracellular Ca(2+) but had no effect on basal or forskolin-
CC stimulated cAMP levels, suggesting that this receptor is G(q)-
CC coupled.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Has a limited expression profile, both
CC peripheral and within the central nervous system, with highest
CC levels in dorsal root ganglion.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.

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DR EMBL, AY042214; AAK91805.1; -
DR EMBL, AB083626; BAB89339.1; -
DR EMBL, AB065811; BAC06030.1; -
DR EMBL, BC063450; AAH63450.1; -
DR MIM: 607228; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P2_1; 1.
KW G-protein coupled receptor; Polymorphism; Transmembrane.
FT DOMAIN 1 33
FT TRANSMEM 34 54 Extracellular (Potential).
FT DOMAIN 55 63 Cytoplasmic (Potential).
FT TRANSMEM 64 84 2 (Potential).
FT DOMAIN 85 96 Extracellular (Potential).
FT TRANSMEM 97 117 3 (Potential).
FT DOMAIN 118 144 Cytoplasmic (Potential).
FT TRANSMEM 145 165 4 (Potential).
FT DOMAIN 166 184 Extracellular (Potential).
FT TRANSMEM 185 205 5 (Potential).
FT DOMAIN 206 228 Cytoplasmic (Potential).
FT TRANSMEM 229 249 6 (Potential).
FT DOMAIN 250 264 Extracellular (Potential).
FT TRANSMEM 265 285 7 (Potential).
FT DOMAIN 286 330 Cytoplasmic (Potential).
FT VARIANT 62 62 N->S (in dbSNP:10833049).
FT VARIANT 62 62 /FTID=VAR_019433.
SQ SEQUENCE 330 AA; 3709 MW; 0B328FD78BDF68B CRC64;
Query Match 5.9%; Score 20; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 7, 6e-11;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
OY 232 TILTLVFLICGLPGIOW 251
DB 224 TILTLVFLICGLPGIOW 243
RESULT 9
AAH63450 PRELIMINARY; PRT; 330 AA.
AC AAH63450;
DT 02-VAR-2004 (TRENBLrel. 27, Created)
DT 02-VAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-VAR-2004 (TRENBLrel. 27, Last annotation update)
DE G protein-coupled receptor MRGX2.
Name=MRGX2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RA MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Krausberg R.D., Collins F.S., Wagner L., Shemen C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton R., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Krausberg R.L.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC063450; AA063450.1; -.
KW Receptor.
SQ SEQUENCE 330 AA; 37099 MW; 0B328FD78B1DF6BE CRC64;
Query Match 5.9%; Score 20; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 7.6e-11; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 232 TILLTVLVLGCLPFGIQW 251
DB 224 TILLTVLVLGCLPFGIQW 243

RESULT 10
MG3 MOUSE STANDARD; PRT; 302 AA.
AC 091MW3;
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Mas-related G-protein coupled receptor member A3.
GN Name=MrgprA3; Synonyms=Mrga3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Dorsal root ganglion;
RX MEDLINE=2145808; PubMed=1151509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of
RT nociceptive sensory neurons.";
RT Cell 106:619-632(2001).
CC -1- FUNCTION: Orphan receptor. May be a receptor for Rfamide-family
CC neuropeptides such as NPFF and NPAF, which are analgesic in vivo.
CC May regulate nociceptor function and/or development, including the
CC sensation or modulation of pain (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that
CC includes nociceptors. Expressed in the subclasses of nonpeptidergic
CC sensory neurons that are IB4(+) and VR1(-).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL, AY042193; AA091789.1; -.
DR MGD; MG12684085; MrgprA3.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001, 7tm1.1.
DR PRINTS, PR00237; GPCRHOOPS.
DR PROSITE, PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE, PS02622; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 17
FT TRANSMEM 18 38
FT TRANSMEM 39 46
FT TRANSMEM 47 67
FT TRANSMEM 68 81
FT TRANSMEM 82 102
FT TRANSMEM 103 129
FT TRANSMEM 130 150
FT TRANSMEM 151 167
FT TRANSMEM 168 188
FT TRANSMEM 189 211
FT TRANSMEM 212 232
FT TRANSMEM 233 242
FT TRANSMEM 243 263
FT TRANSMEM 264 302
FT CARBOHYD 2 2
FT CARBOHYD 68 68
FT CARBOHYD 159 159
SQ SEQUENCE 302 AA; 34483 MW; 8E4CC023AC02B5E5 CRC64;
Query Match 4.5%; Score 15; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 GLSMIAISTERTCLS 138
DB 98 GLSMIAISTERTCLS 112

RESULT 11
MG1 MOUSE STANDARD; PRT; 304 AA.
AC 091MW5;
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Mas-related G-protein coupled receptor member A1 (Rfamide G protein-
DE coupled receptor).
GN Name=MrgprA1; Synonyms=Mrga1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Dorsal root ganglion;
RX MEDLINE=2145808; PubMed=1151509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of
RT nociceptive sensory neurons.";
RT Cell 106:619-632(2001).
CC -1- FUNCTION: Orphan receptor. May be a receptor for Rfamide-family
CC neuropeptides such as NPFF and NPAF, which are analgesic in vivo.
CC May regulate nociceptor function and/or development, including the
CC sensation or modulation of pain.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that
CC includes nociceptors. Expressed in the subclasses of nonpeptidergic
CC sensory neurons that are IB4(+) and VR1(-).
CC -----
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CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Was subfamily.
 CC -----
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 CC -----
 CC EMBL, AY042191; AAK31787.1; --
 CC WCD; MG1:3033095; Mrgpr1.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm1.1.
 CC PRINTS: PR00237; GPCRHOOPS.
 CC PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Glycoprotein; Transmembrane.
 CC DOMAIN 1 17
 CC TRANSMEM 18 38
 CC DOMAIN 39 53
 CC TRANSMEM 54 74
 CC DOMAIN 75 75
 CC TRANSMEM 76 96
 CC DOMAIN 97 131
 CC TRANSMEM 132 152
 CC DOMAIN 153 167
 CC TRANSMEM 167 188
 CC DOMAIN 188 206
 CC TRANSMEM 207 223
 CC DOMAIN 228 244
 CC TRANSMEM 244 264
 CC DOMAIN 265 304
 CC CARBOHYD 10 10
 CC SEQUENCE 304 AA; 34381 MW; C56CBF879067A52B CRC64;
 CC
 CC Query Match 4.5%; Score 15; DB 1; Length 304;
 CC Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 124 GLSMLSAISTERCLS 138
 CC Db 97 GLSMLSAISTERCLS 111
 CC
 CC RESULT 12
 CC MRCG_RAT STANDARD; PRT; 304 AA.
 CC ID MRCG_RAT
 CC AC 07TN49;
 CC DT 01-OCT-2004 (Rel. 45, Created)
 CC DT 01-OCT-2004 (Rel. 45, Last sequence update)
 CC DT 01-OCT-2004 (Rel. 45, Last annotation update)
 CC DB Mas-related G-protein coupled receptor member A.
 CC GN Name=Mrgpra; Synonyms=Mrga;
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Sprague-Dawley;
 CC RX MEDLINE=22810130; PubMed=12909716; DOI=10.1073/pnas.1732949100;
 CC RA Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
 CC RT "Atypical expansion in mice of the sensory neuron-specific Mrg G
 CC protein-coupled receptor family."
 CC RL Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
 CC -1- FUNCTION: Orphan receptor. May regulate nociceptor function and/or
 CC development, including the sensation or modulation of pain.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Was subfamily.
 CC -----

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, AF518238; AAC08310.1; --
 CC RGD; 738050; Mrgpra.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm1.1.
 CC PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane.
 CC DOMAIN 1 17
 CC TRANSMEM 18 38
 CC DOMAIN 39 46
 CC TRANSMEM 47 67
 CC DOMAIN 68 80
 CC TRANSMEM 81 101
 CC DOMAIN 102 132
 CC TRANSMEM 133 153
 CC DOMAIN 154 167
 CC TRANSMEM 168 188
 CC DOMAIN 189 211
 CC TRANSMEM 212 232
 CC DOMAIN 233 244
 CC TRANSMEM 245 265
 CC DOMAIN 266 304
 CC SEQUENCE 304 AA; 34334 MW; 4A8204A80192E8B6 CRC64;
 CC
 CC Query Match 4.5%; Score 15; DB 1; Length 304;
 CC Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 124 GLSMLSAISTERCLS 138
 CC Db 98 GLSMLSAISTERCLS 112
 CC
 CC RESULT 13
 CC M7A7_MOUSE STANDARD; PRT; 305 AA.
 CC ID M7A7_MOUSE
 CC AC Q912C5;
 CC DT 01-OCT-2004 (Rel. 45, Created)
 CC DT 01-OCT-2004 (Rel. 45, Last sequence update)
 CC DT 01-OCT-2004 (Rel. 45, Last annotation update)
 CC DB Mas-related G-protein coupled receptor member A7.
 CC GN Name=Mrgpra7; Synonyms=Mrga7;
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 CC RC STRAIN=129/SvJ;
 CC RX MEDLINE=21435808; PubMed=11551509;
 CC RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
 CC RT "A diverse family of GPCRs expressed in specific subsets of
 CC nociceptive sensory neurons."
 CC RL Cell 106:619-632(2001).
 CC -1- FUNCTION: Orphan receptor. May be a receptor for Rfam1de-family
 CC neuropeptides such as NPF and NPAF, which are analgesic in vivo.
 CC May regulate nociceptor function and/or development, including the
 CC sensation or modulation of pain (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that
 CC includes nociceptors. Expressed in the subclass of nonpeptidergic
 CC sensory neurons that are IB4(+) and VR1(-).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Was subfamily.
 CC -----

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DR EMBL: AY042197; AKG91793.1; -
DR MGD; MG1:3033109; Mrgpra7.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 17 Extracellular (Potential).
FT TRANSMEM 18 38 1 (Potential).
FT DOMAIN 39 46 Cytoplasmic (Potential).
FT TRANSMEM 47 67 2 (Potential).
FT DOMAIN 68 81 Extracellular (Potential).
FT TRANSMEM 82 102 3 (Potential).
FT DOMAIN 103 129 Cytoplasmic (Potential).
FT TRANSMEM 130 150 4 (Potential).
FT DOMAIN 151 167 Extracellular (Potential).
FT TRANSMEM 168 188 5 (Potential).
FT DOMAIN 189 211 Cytoplasmic (Potential).
FT TRANSMEM 212 232 6 (Potential).
FT DOMAIN 233 244 Extracellular (Potential).
FT TRANSMEM 245 265 7 (Potential).
FT DOMAIN 266 305 Cytoplasmic (Potential).
SQ SEQUENCE 305 AA; 35034 MW; 2544FD3B9B9ED39 CRC64;

Query Match 4.5%; Score 15; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 GLSMLSAISTERCLS 138
Db 98 GLSMLSAISTERCLS 112

RESULT 14
MGAB_MOUSE
ID MGAB_MOUSE STANDARD; PRT; 305 AA.
AC G91ZC4;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Mas-related G-protein coupled receptor member A8.
GN Name=Mrgpra8; Synonyms=Mrga8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylika M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of
RL nociceptive sensory neurons.";
Cell 106:619-632(2001).
CC -1- FUNCTION: Orphan receptor. May be a receptor for Rfamide-family
CC neuropeptides such as NPPF and NPAF, which are analgesic in vivo.
CC May regulate nociceptor function and/or development, including the
CC sensation or modulation of pain (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that
CC includes nociceptors. Expressed in the subulass of nonpeptidergic
CC sensory neurons that are IB4(+) and VR1(-).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.

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DR EMBL: AY042198; AKG91794.1; -
DR MGD; MG1:3033111; Mrgpra8.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 17 Extracellular (Potential).
FT TRANSMEM 18 38 1 (Potential).
FT DOMAIN 39 46 Cytoplasmic (Potential).
FT TRANSMEM 47 67 2 (Potential).
FT DOMAIN 68 85 Extracellular (Potential).
FT TRANSMEM 86 106 3 (Potential).
FT DOMAIN 107 129 Cytoplasmic (Potential).
FT TRANSMEM 130 150 4 (Potential).
FT DOMAIN 151 172 Extracellular (Potential).
FT TRANSMEM 173 193 5 (Potential).
FT DOMAIN 194 207 Cytoplasmic (Potential).
FT TRANSMEM 208 228 6 (Potential).
FT DOMAIN 229 243 Extracellular (Potential).
FT TRANSMEM 244 264 7 (Potential).
FT DOMAIN 265 305 Cytoplasmic (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 305 AA; 35004 MW; D6BB232DA58534F CRC64;

Query Match 4.5%; Score 15; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 GLSMLSAISTERCLS 138
Db 98 GLSMLSAISTERCLS 112

RESULT 15
MGAB_MOUSE
ID MGAB_MOUSE STANDARD; PRT; 313 AA.
AC G91WZ2;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Mas-related G-protein coupled receptor member A4 (RF-amide G protein-
DE coupled receptor).
GN Name=Mrgpra4; Synonyms=Mrga4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Dorsal root ganglion;
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylika M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of
RL nociceptive sensory neurons.";
Cell 106:619-632(2001).
CC -1- FUNCTION: Orphan receptor. May be a receptor for Rfamide-family
CC neuropeptides such as NPPF and NPAF, which are analgesic in vivo.
CC May regulate nociceptor function and/or development, including the
CC sensation or modulation of pain.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that

```
CC includes nociceptors. Expressed in the subclass of nonpeptidergic
CC sensory neurons that are IB4(+) and VR1(-).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Mas subfamily.
-----
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-----
CC
DR EMBL; AY042194; AAK91790.1; -.
DR MGD; MGI:3033100; Mrp4.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GFCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Glycoprotein; Transmembrane.
PT DOMAIN 1 25 Extracellular (Potential).
PT TRANSMEM 26 46 1 (Potential).
PT DOMAIN 47 54 Cytoplasmic (Potential).
PT TRANSMEM 55 75 2 (Potential).
PT DOMAIN 76 93 Extracellular (Potential).
PT TRANSMEM 94 114 3 (Potential).
PT DOMAIN 115 137 Cytoplasmic (Potential).
PT TRANSMEM 138 158 4 (Potential).
PT DOMAIN 159 182 Extracellular (Potential).
PT TRANSMEM 183 203 5 (Potential).
PT DOMAIN 204 219 Cytoplasmic (Potential).
PT TRANSMEM 220 240 6 (Potential).
PT DOMAIN 241 255 Extracellular (Potential).
PT TRANSMEM 256 276 7 (Potential).
PT DOMAIN 277 313 Cytoplasmic (Potential).
FT CARBOHYD 10 10 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 76 76 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 313 AA; 35667 MW; 22F3AEC2F2F7127B CRC64;
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Query Match 4.5%; Score 15; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 124 GLSMLSAISTERCLS 138
|||
Db 106 GLSMLSAISTERCLS 120

Search completed: October 27, 2004, 08:51:36
Job time : 197 secs

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OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 10:19:03 ; Search time 215 Seconds
(without alignments)

8655.094 Million cell updates/sec

Title: US-09-867-570-1

Perfect score: 2618
Sequence: 1 aacaatgcgcgcgaattcgcg.....gaaaaaaaaaaaaaaaaa 2618

Scoring table: IDENTITY_NUC
Gap 10.0 , Gape 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949.8	36.3	969	US-09-254-227A-4	Sequence 4, Appl1
2	938.6	35.9	969	US-09-254-227A-6	Sequence 6, Appl1
3	836.2	31.9	969	US-09-254-227A-12	Sequence 12, Appl1
4	833	31.8	969	US-09-254-227A-8	Sequence 8, Appl1
5	829.8	31.7	969	US-09-254-227A-14	Sequence 14, Appl1
6	826.6	31.6	969	US-09-254-227A-10	Sequence 10, Appl1
7	410.2	15.7	1011	US-09-254-227A-2	Sequence 2, Appl1
8	291	11.1	291	US-09-495-050A-164	Sequence 164, App
9	275	10.5	275	US-09-016-434-330	Sequence 330, App
C 10	146.4	5.6	148567	US-09-801-876B-3	Sequence 3, Appl1
C 11	146.4	5.6	148567	US-10-254-869-3	Sequence 3, Appl1
C 12	132.2	5.0	12047	US-09-033-556-3	Sequence 1, Appl1
C 13	132.2	5.0	12047	US-09-033-556-3	Sequence 1, Appl1
C 14	132.2	5.0	12047	US-09-474-699-11	Sequence 4, Appl1
C 15	132.2	5.0	12047	US-09-151-376-3	Sequence 3, Appl1
C 16	132.2	5.0	12047	US-09-814-351-11	Sequence 11, Appl1
C 17	126.8	4.8	118067	US-09-497-855A-32	Sequence 32, Appl1
C 18	123.4	4.7	11288	US-08-646-301A-1	Sequence 1, Appl1
C 19	123.4	4.7	11288	US-08-481-968A-4	Sequence 4, Appl1
C 20	123.4	4.7	11288	US-08-154-712B-4	Sequence 4, Appl1
C 21	123.4	4.7	11288	US-09-947-925A-4	Sequence 4, Appl1
C 22	123.4	4.7	15056	US-09-474-699-10	Sequence 10, Appl1
C 23	123.4	4.7	15056	US-09-814-351-14	Sequence 14, Appl1
C 24	122.8	4.7	14364	US-10-067-443-20	Sequence 20, Appl1
C 25	120.6	4.6	45716	US-08-965-048-5	Sequence 5, Appl1
C 26	120.6	4.6	45989	US-08-965-048-6	Sequence 6, Appl1
C 27	118.6	4.5	1388	US-09-016-434-1225	Sequence 1225, Ap

C 28	118.6	4.5	1388	5	PCT-US93-06251-26	Sequence 26, Appl1
C 29	114.4	4.4	3216	2	US-08-828-007-1	Sequence 1, Appl1
C 30	114.4	4.4	3216	2	US-09-513-999C-25490	Sequence 25490, A
C 31	113.2	4.3	44453	3	US-09-146-053-5	Sequence 5, Appl1
C 32	112	4.3	505	3	US-09-227-357-73	Sequence 73, Appl1
C 33	111.6	4.3	1000	4	US-09-671-317-221	Sequence 221, App
C 34	111.6	4.3	1001	4	US-09-671-317-219	Sequence 219, App
C 35	111.6	4.3	1001	4	US-09-671-317-220	Sequence 220, App
C 36	111.6	4.3	1001	4	US-09-671-317-222	Sequence 222, App
C 37	110.8	4.2	2435	4	US-09-484-970B-134	Sequence 134, App
C 38	105.4	4.0	152331	3	US-09-128-155-16	Sequence 16, Appl1
C 39	105.4	4.0	176373	3	US-09-128-155-17	Sequence 17, Appl1
C 40	105	4.0	54945	4	US-09-967-669-10	Sequence 10, Appl1
C 41	104.4	4.0	152331	3	US-09-128-155-16	Sequence 16, Appl1
C 42	103.6	4.0	319608	4	US-09-539-333D-1	Sequence 1, Appl1
C 43	103.6	4.0	319608	4	US-09-679-409-18282	Sequence 1, Appl1
C 44	103.4	3.9	438	2	US-09-621-976-18282	Sequence 18282, A
C 45	102.6	3.9	246240	2	US-08-724-394A-20	Sequence 20, Appl1

ALIGNMENTS

RESULT 1									
US-09-254-227A-4									
Sequence 4, Application US/09254227A									
Patent No. 6696257									
GENERAL INFORMATION:									
APPLICANT: Ahmad, Sultan									
APPLICANT: Banville, Denis									
APPLICANT: Fortin, Yves									
APPLICANT: Lembo, Paola									
APPLICANT: O'Donnell, Dajan									
APPLICANT: Shi-Hsiang, Shen									
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human									
FILE REFERENCE: 81823/268117									
CURRENT APPLICATION NUMBER: US/09/254,227A									
CURRENT FILING DATE: 1999-03-03									
NUMBER OF SEQ ID NOS: 22									
SOFTWARE: PatentIn version 3.0									
SEQ ID NO 4									
LENGTH: 969									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-254-227A-4									
Query Match									
Best Local Similarity 98.8%; Pred. No. 2,2e-263;									
Matches 957; Conservative 0; Mismatches 12; Indels 0; Gaps 0;									
QY	492	ATGATTCACACCATCCAGTCTTGAGTACAGAACTGACACCAATCAACGACGAGAG	551						
DB	1	ATGATTCACACCATCCAGTCTTGAGTACAGAACTGACACCAATCAACGACGAGAG	60						
QY	552	ACTGCTGTACACGACGAGCCTGAGCTTACGCGGCGTGAAGTATGCTTCCCTTGTG	611						
DB	61	ACTGCTGTACACGACGAGCCTGAGCTTACGCGGCGTGAAGTATGCTTCCCTTGTG	120						
QY	612	CGCGTGAAGAAACGGGTTGTGCTGTGCTCTGAGCTTGCGGATGCGGAGAGCT	671						
DB	121	CGCGTGAAGAAACGGGTTGTGCTGTGCTCTGAGCTTGCGGATGCGGAGAGAGCT	180						
QY	672	GTCCTCATTCACATCCCTCAACCTGCTGCGGCGCACTTCTCTTCTTAAGGCGCACTT	731						
DB	181	GTCCTCATTCACATCCCTCAACCTGCTGCGGCGCACTTCTCTTCTTAAGGCGCACTT	240						
QY	732	ATATGTTGCGCGTACCGCTCATATATCGGATCCCATCTCCAAATCTCGATCTCT	791						
DB	241	ATATGTTGCGCGTACCGCTCATATATCGGATCCCATCTCCAAATCTCGATCTCT	300						
QY	792	GTCATGACCTTTCCCTTATATGAGCGCTTAAGCATGTGTCGAGCGCATCAGCACCGAGCGC	851						
DB	301	GTCATGACCTTTCCCTTATATGAGCGCTTAAGCATGTGTCGAGCGCATCAGCACCGAGCGC	360						

QY 852 TGCGTGTGATTCCTGTGGGCGCATCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 911
DB 361 TGCGGTGTGATTCCTGTGGGCGCATCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 420
QY 912 GTGATGTGTGCTGCTGTGGGCGCATCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 971
DB 421 GTGATGTGTGCTGCTGTGGGCGCATCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 480
QY 972 TGATGATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1031
DB 481 TGATGATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 540
QY 1032 ATGCGGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1091
DB 541 ATGCGGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 600
QY 1092 AGATATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1151
DB 601 AGATATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 660
QY 1152 ACAGTGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1211
DB 661 ACAGTGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 720
QY 1212 AGATATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1271
DB 721 AGATATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 780
QY 1272 TCAGTGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1331
DB 781 TCAGTGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 840
QY 1332 CGTCAAAATGAGCAGAACTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1391
DB 841 CGTCAAAATGAGCAGAACTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 900
QY 1392 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1451
DB 901 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 960
QY 1452 GAGCAGTGA 1460
DB 961 GAGCAGTGA 969

RESULT 2

US-09-254-227A-6
Sequence 6, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
US-09-254-227A-6

Query Match 35.9%; Score 938.6; DB 4; Length 969;
Best Local Similarity 98.0%; Pred. No. 3.7e-260;
Matches 950; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 492 ATGATTTACCACTCCAGTCTTGGGTACAGAACTGACAACTCAACGACGATGAGAG 551
DB 1 ATGATTTACCACTCCAGTCTTGGGTACAGAACTGACAACTCAACGACGATGAGAG 60
QY 552 ACTCTGTGCTACAGACAGACCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 611
DB 61 ACTCTGTGCTACAGACAGACCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 120
QY 612 GCGGTGACAGAAAGCGGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 671
DB 121 GCGGTGACAGAAAGCGGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 180
QY 672 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 731
DB 181 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 240
QY 732 ATATGTGACGCTTACGCTCATCAATATCCGACATCCATCTCCAAATCTCAGTCTCT 791
DB 241 ATATGTGACGCTTACGCTCATCAATATCCGACATCCATCTCCAAATCTCAGTCTCT 300
QY 792 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 851
DB 301 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 360
QY 852 TGCGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 911
DB 361 TGCGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 420
QY 912 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 971
DB 421 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 480
QY 972 TGATGATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1031
DB 481 TGATGATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 540
QY 1032 ATGCGGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1091
DB 541 ATGCGGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 600
QY 1092 AGATATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1151
DB 601 AGATATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 660
QY 1152 ACAGTGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1211
DB 661 ACAGTGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 720
QY 1212 AGATATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1271
DB 721 AGATATTCCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 780
QY 1272 TCAGTGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1331
DB 781 TCAGTGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 840
QY 1332 CGTCAAAATGAGCAGAACTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1391
DB 841 CTTCAAAATGAGCAGAACTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 900
QY 1392 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 1451
DB 901 GTGATGTGTGCTGTGTAGTGTGCTGTGATCACTGCGCGCGCCGAGATACCTGTGATCG 960
QY 1452 GAGCAGTGA 1460
DB 961 GAGCAGTGA 969

RESULT 3

US-09-254-227A-12
Sequence 12, Application US/09254227A
Patent No. 6696257

GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent in version 3.0
SEQ ID NO 12
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
US-09-254-227A-12

Query Match 31.8%; Score 836.2; DB 4; Length 969;
Best Local Similarity 91.4%; Pred. No. 1.2e-230;
Matches 886; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 492 ATGATTCACACATCCAGTCTTGGGTAACAGAACTGACACCAATCAACGAGCTGAGAG 551
DB 1 ATGATTCACACCGTCCAGTCTTGGGTAACAAATCGACACCAATCAACGAGCTGAGAG 60
QY 552 ACTCTTGTCTACAGAGACCTTACAGCTTACAGGAGCTGAGAGCTTCCCTTGTG 611
DB 61 ACTCTTGTCTACAGAGACCTTACAGCTTACAGGAGCTGAGAGCTTACATTTCCCTTGTG 120
QY 612 GCGCTGACAGAAACGCGGTTGTCTGCTGCTGCGGCTGCGCATGCGGAGAGAGCT 671
DB 121 GAGCTGACAGAAACGCGGTTGTCTGCTGCTGCGGCTGCGCATGCGGAGAGAGCT 180
QY 672 GTCCTCATCTACATCTCAACCTGCTGCGGCTGCGCATCTTCTTCTTACGCGCACAAT 731
DB 181 GTCCTCATCTACATCTCAACCTGCTGCGGCTGCGCATCTTCTTCTTACGCGCACAAT 240
QY 732 ATATGTTGCGCGTTACGCTTATATGAGCTTAAAGCTGAGAGGCGCATGAGAGAGAG 791
DB 241 ATATGTTGCGCGTTACGCTTATATGAGCTTAAAGCTGAGAGGCGCATGAGAGAGAG 300
QY 792 GTATGACCTTTCCTTATATGAGCTTAAAGCTGAGAGGCGCATGAGAGAGAGAG 851
DB 301 GTATGACCTTTCCTTATATGAGCTTAAAGCTGAGAGGCGCATGAGAGAGAGAG 360
QY 852 TGCCTGTCATCTGAGGCGCATGAGAGGCGCATGAGAGGCGCATGAGAGAGAG 911
DB 361 TGCCTGTCATCTGAGGCGCATGAGAGGCGCATGAGAGGCGCATGAGAGAGAG 420
QY 912 GTATGAGTGTCTGCTGCTGAGGCGCTGCTGCTGCTGCGGAGATGCTGAGAGAG 971
DB 421 GTATGAGTGTCTGCTGCTGAGGCGCTGCTGCTGCTGCTGCTGAGAGAGAGAG 480
QY 972 TGTGACCTTCCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 1031
DB 481 TGTGACCTTCCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 540
QY 1032 ATGCGCTGAGCTTATATGAGTGTCTGAGGCTGAGGCTGAGGCTGAGGCT 1091
DB 541 GTGCGGAGGCTGAGTATATGAGTGTCTGAGGCTGAGGCTGAGGCTGAGGCT 600
QY 1092 AGATTTCTGTGAGATCCGAGAGATGCGGCTGAGAGGCTGAGAGGCTGAG 1151
DB 601 AGATTTCTGTGAGATCCGAGAGATGCGGCTGAGAGGCTGAGAGGCTGAG 660
QY 1152 ACAGTGTGAGTCTCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1211
DB 661 ACAGTGTGAGTCTCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 720
QY 1212 AGATTCACCTGAGTGAAGTCTTATTTGATGATGATCTGATTTCCATTTTCTG 1271

DB 721 AGATTCACCTGAGTGAAGTCTTATTTGATGATGATCTGATTTCCATTTTCTG 780
QY 1272 TCGCTCTTAAACAGAGGCGCAACCCCATCATTTACTTCTTCTGAGGCTCTTTAGGAG 1331
DB 781 TCGCTCTTAAACAGAGTGTGCAACCCCATCATTTACTTCTTCTGAGGCTCTTTAGGAG 840
QY 1332 CGTCAAAATAGGAGAACTGAGAGCTTCTCCAGAGGCTCTGAGAGAGAGCTGAG 1391
DB 841 CGTCAAAATAGGAGAACTGAGAGCTTCTCCAGAGGCTCTGAGAGAGAGAGCTGAG 900
QY 1392 GTGATGAAGTGAAGGCTGCTTCTCCAGAGAACTTGAAGCTGTGAGAGAGAGATG 1451
DB 901 GTGATGAAGTGAAGGCTGCTTCTCCAGAGAACTTGAAGCTGTGAGAGAGAGATG 960
QY 1452 GAGCAGTGA 1460
DB 961 GAGCAGTGA 969

RESULT 4
US-09-254-227A-8
Sequence 8, Application US/09254227A
Patent No. 696257

GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent in version 3.0
SEQ ID NO 8
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
US-09-254-227A-8

Query Match 31.8%; Score 833; DB 4; Length 969;
Best Local Similarity 91.2%; Pred. No. 1e-229;
Matches 884; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 492 ATGATTCACACATCCAGTCTTGGGTAACAGAACTGACACCAATCAACGAGCTGAGAG 551
DB 1 ATGATTCACACCGTCCAGTCTTGGGTAACAAATCGACACCAATCAACGAGCTGAGAG 60
QY 552 ACTCTTGTCTACAGAGACCTTACAGCTTACAGGAGCTGAGAGCTTCCCTTGTG 611
DB 61 ACTCTTGTCTACAGAGACCTTACAGCTTACAGGAGCTGAGAGCTTACATTTCCCTTGTG 120
QY 612 GCGCTGACAGAAACGCGGTTGTCTGCTGCTGCGGCTGCGCATGCGGAGAGAGCT 671
DB 121 GAGCTGACAGAAACGCGGTTGTCTGCTGCTGCGGCTGCGCATGCGGAGAGAGCT 180
QY 672 GTCCTCATCTACATCTCAACCTGCTGCGGCTGCGCATCTTCTTCTTACGCGCACAAT 731
DB 181 GTCCTCATCTACATCTCAACCTGCTGCGGCTGCGCATCTTCTTCTTACGCGCACAAT 240
QY 732 ATATGTTGCGCGTTACGCTTATATGAGCTTAAAGCTGAGAGGCGCATGAGAGAGAG 791
DB 241 ATATGTTGCGCGTTACGCTTATATGAGCTTAAAGCTGAGAGGCGCATGAGAGAGAG 300
QY 792 GTATGACCTTTCCTTATATGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 1031
DB 301 GTATGACCTTTCCTTATATGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 540
QY 1032 ATGCGCTGAGCTTATATGAGTGTCTGAGGCTGAGGCTGAGGCTGAGGCT 1091
DB 541 GTGCGGAGGCTGAGTATATGAGTGTCTGAGGCTGAGGCTGAGGCTGAGGCT 600
QY 1092 AGATTTCTGTGAGATCCGAGAGATGCGGCTGAGAGGCTGAGAGGCTGAG 1151
DB 601 AGATTTCTGTGAGATCCGAGAGATGCGGCTGAGAGGCTGAGAGGCTGAG 660
QY 1152 ACAGTGTGAGTCTCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1211
DB 661 ACAGTGTGAGTCTCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 720
QY 1212 AGATTCACCTGAGTGAAGTCTTATTTGATGATGATCTGATTTCCATTTTCTG 1271

APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Heiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
US-09-254-227A-10

Query Match 31.6%; Score 826.6; DB 4; Length 969;
Best Local Similarity 90.8%; Pred. No. 7.2e-228;
Matches 880; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

492 ATGATTCACACATCCAGTCTGGGTACAGAACTGACCAATCAACGAGCGAGAG 551
1 ATGATTCACACGCTTCACTTGAACAAGAAATGACCAATCAACGAGCGAGAG 60
552 ACTCTTGTCTACAGACAGACCTGAGCTTCAAGGAGCTGACGTCATGTTCCCTTGTG 611
61 ACTTTTGTCTACAGACAGACCTTGAAGCTTCAAGGAGCTGACGTCATGTTCCCTTGTG 120
612 GCGCTGACAGAAACGGGTTGCTCTGCTCTGAGGCTGCGCATGCGAGAGAGCT 671
121 GGGCTGACAGAAACGGGTTGCTCTGCTCTGAGGCTGCGCATGCGAGAGAGCT 180
672 GTCCTCATCTACATCTCAACCTGCTGCGGCGGAGCTTCCCTTCAAGGCGCAGATT 731
181 TTCTCACTACATCTCAACCTGCTGCGGCGGAGCTTCCCTTCAAGGCGCAGATT 240
732 ATATGTCGCGCTTACCGCTCATATATCCGACATCCCATCTCAAAATCTCTAGTCT 791
241 ATATATTCCTGTTAAGCTTATCAATATCCCATATCCCATATCTTAAATCTCTATCT 300
792 GTGATGACCTTTTCCCTTATATAGGCTTAAAGCTGATGAGCGCATGACAGACGAGCG 851
301 GTGATGATGTTTCTTCTTCTTGAAGCTTGAAGCTTCTGATGCGGAGACAGAGCGCG 360
852 TGCTGTGACATCTGATGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 911
361 TGCTGTGACATCTGATGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 420
912 GTGATGATGCTGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
421 GTGATGATGCTGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
972 TGATGATCTCTGTTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1031
481 TGATGATCTCTGTTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 540
1032 ATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
541 GTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
1092 AGATTTCTGATGATCCCGAAGATGCGGCTGACAGAGCTGATGATGATGATGATGAT 1151
601 AGATTTCTGATGATCCCGAAGATGCGGCTGACAGAGCTGATGATGATGATGATGAT 660
1152 ACAGTGTGATCTTCTCTCTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
661 ACAGTGTGATCTTCTCTCTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
1212 AGATTCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1271
721 TGATTCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
1272 TCGGCTTAAACAGAGTGCACACCCATCAATTAATCTTCTGAGGCTCTTAAAGGAG 1331

Db 781 TCGGCTTAAACAGAGTGCACACCCATCAATTAATCTTCTGAGGCTCTTAAAGGAG 840
Qy 1332 CGTCAAAATAGGAGAGAACTGAAGCTGTTCTCCAGAGGCTCTGACAGACAGCTGAG 1391
Db 841 CGTCAAAATAGGAGAGAACTGAAGCTGTTCTCCAGAGGCTCTGACAGAGCTGAG 900
Qy 1392 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1451
Db 901 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Qy 1452 GAGCAGTGA 1460
Db 961 GAGCAGTGA 969

RESULT 7
US-09-254-227A-2
Sequence 2, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Heiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1011
TYPE: DNA
ORGANISM: rat
US-09-254-227A-2

Query Match 15.7%; Score 410.2; DB 4; Length 1011;
Best Local Similarity 65.6%; Pred. No. 8.4e-108;
Matches 655; Conservative 0; Mismatches 333; Indels 21; Gaps 3;

466 GGGTCATCAGACTGGGCTTCTGAGCATGATTCACATCCAGTCTTGGGTACAGAAC 525
17 GGGACACTCAGAGAAATTTGTAGCATGATTCACATCTCATCTCCTAGTACAGAT 76
526 TGACCAATCAACGAGAGTGAAGAGACTCTTGTCTAACAGACAGCTTGAAGCTTCAAG 585
77 CTACACACTGAAATTAATAGTGTCA---TCCAGTTGACAGGCAATCTCACTCTGCT 133
586 GGTGACGTGATGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
134 TCCGTGCTCCATCATATCACTGCTGATGATGAGAGAAACACATGTAATCTGAGCTCT 193
646 TGAGCTGCGGATGCGAGAGAGCTGCTCATCTCATCTCATCTCATCTCATCTCATCT 705
194 TGAGATTCGAGATGCGAGAGAGAGCTCATCTCATCTCATCTCATCTCATCTCATCT 253
706 ACTTCTCTTCTTAAAGGCGGACATTAATGTTGCGGTTAAGCT----- 751
254 ACTCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 313
752 -CATCATATCCGATCCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 810
314 GCATCTATGCGCATTAATTAAGCAAGAAATCTTAAGCAATGATGATCAATCTCTATA 373
811 TTATAGGCTTAAGCATGCTGAGCGCATGACAGACAGAGCTGCTGCTGCTGCTGCTGCT 870
374 TCTAGGCTGAGCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 433
871 CCATCTGATACACTGCTGCGCGCGCCAGATACCTGATGATGATGATGATGATGATGAT 930
434 CAATCTGATACACTGCTGCGCGCGCCAGATACCTGATGATGATGATGATGATGATGAT 493

QY 931 GGGCCCTGTCCTGCTGCGAGATATCTGAGTGAATGTTCTGTGAATTCCTGTTTAGTG 990
DB 494 GGGTCTCTCTCTCTCTCAATGAGCATCTGATGAGTTTCTCAGGATTCCTG--GGTG 550
QY 991 GTGCTGATTCCTGTTGCTGTAAGTCAAGTATTCATTAACATCGGTGGCTGTTTCTT 1050
DB 551 AGACTCAGCATCATTTGTTGGAATAAATGTTGACTTAAATGTAATGATTTGATTTTCT 610
QY 1051 TATGATGATTCCTGTTGAGTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1110
DB 611 TATTTATCTCTCTCTCTGAGTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 670
QY 1111 GGAAGATGCGCTGACCAAGCTGTACGTGACCAATCTCTCAAGTGTCTGCTCTCC 1170
DB 671 GACGGAACCACTGTCAGGCTGTAGTACATCTCTCAAGATGATGCTACCTCA 730
QY 1171 TCTGTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1230
DB 731 TCTGTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 790
QY 1231 AAGTCTTATTTGTCATGTCATAGTATTCATTTCTGTCCTGCTGCTGCTGCTGCTG 1290
DB 791 ATTATCTCTTTTGTCAATTTACAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTG 850
QY 1291 CCAACCCCATCATTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1350
DB 851 CCAACCCCATCATTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 910
QY 1351 TGAAGCTGCTTCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1410
DB 911 TCAAAATGCTTCTTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
QY 1411 GCTTCTCTCAGAAACCTGAGCTGTGCGGAAGCAT 1449
DB 971 GCCATGTTCAAGAACCTCACTGATCTCAGAAAGAGAT 1009

RESULT 8
US-09-495-050A-164
Sequence 164, Application US/09495050A
Patent No. 6492505
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED H
FILE REFERENCE: PA-0013 US
CURRENT APPLICATION NUMBER: US/09/495,050A
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 164
LENGTH: 291
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6492505 1909132CT1
US-09-495-050A-164

Query Match 11.1%; Score 291; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 8.5e-74;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 CGCCATCCCATCTCCAAATCTCTGATGATGATGATGATGATGATGATGATGATGAT 821
DB 1 CGCCATCCCATCTCCAAATCTCTGATGATGATGATGATGATGATGATGATGATGAT 60
QY 822 AGCATGCTGAGGCGCATGACGACCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 881

DB 61 AGCATGCTGAGGCGCATGACGACCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 882 CACTGCGCGCGCGCGCGAGATACCTGTCATGCTGATGCTGCTGCTGCTGCTGCTGCTG 941
DB 121 CACTGCGCGCGCGCGCGAGATACCTGTCATGCTGATGCTGCTGCTGCTGCTGCTGCTG 180
QY 942 CTGCTGCGGAGTATCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1001
DB 181 CTGCTGCGGAGTATCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 1002 GTTGTGATGAAAGCTCAGATTTCTATTAATGCGGCTGCTGCTGCTGCTGCTGCT 1052
DB 241 GTTGTGATGAAAGCTCAGATTTCTATTAATGCGGCTGCTGCTGCTGCTGCTGCT 291

RESULT 9
US-09-016-434-330
Sequence 330, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 330:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CONNUTU01
CLONE: 1909132
US-09-016-434-330

Query Match 10.5%; Score 275; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 3.4e-69;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 CGCCATCCCATCTCCAAATCTCTGATGATGATGATGATGATGATGATGATGATGAT 821
DB 1 CGCCATCCCATCTCCAAATCTCTGATGATGATGATGATGATGATGATGATGATGAT 60
QY 822 AGCATGCTGAGGCGCATGACGACCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 881

REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20003.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12047 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-022-461-1

Query Match 5.0%; Score 132.2; DB 2; Length 12047;
Best Local Similarity 75.9%; Pred. No. 6.2e-27;
Matches 189; Conservative 0; Mismatches 58; Indels 2; Gaps 2;

QY 28 TGAATCTAGTGTGTTAAAGGCTGAGACCTCTCCCTCTCTTACTCTGCTCTCA 87
DB 5320 TGAATCTAGTGTGTTAAAGGCTGAGACCTCTCCCTCTCTTACTCTGCTCTCA 87
QY 88 CCATGTGAGACGCTCGCTCCCTCTTGCCTTACACGAGATTGGAAGCTTCTGAGGCC 147
DB 5380 CCATGTGAGATACCT-GCTCCGCTTTGCTTCTACATAGTAAAGCCCTGAGGCC 5438
QY 148 TCCCGAGAAGAGAGCTGCTATGCTTCTGTACAGCTGTAGAGCTATTAGCCAGTTAA 207
DB 5439 TCCCGAGAAGAGAGCTGCTATGCTTCTGTACAGCTGTAGAGCTATTAGCCAGTTAA 5498
QY 208 ACCCATCTCTCATTAATTTCCAGCTCAGGATTTCTTTTGAACAATTGAGATGA 267
DB 5499 ACCCTCTTCTGTATATA-TTACAGCTGTGAGTATCTCTTACAGCAGTGTGAGAACG 5557
QY 268 ACTAATACA 276
DB 5558 ACTAATACA 5566

RESULT 13

US-09-033-556-3
Sequence 3, Application US/09033556
Patent No. 6432700
GENERAL INFORMATION:
APPLICANT: Henderson, Daniel R.
APPLICANT: Yu, De Chao
TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
TITLE OF INVENTION: HERPETOGENUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: OF USING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,556
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20010.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12047 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-033-556-3

Query Match 5.0%; Score 132.2; DB 4; Length 12047;
Best Local Similarity 75.9%; Pred. No. 6.2e-27;
Matches 189; Conservative 0; Mismatches 58; Indels 2; Gaps 2;

QY 28 TGAATCTAGTGTGTTAAAGGCTGAGACCTCTCCCTCTCTTACTCTGCTCTCA 87
DB 5320 TGAATCTAGTGTGTTAAAGGCTGAGACCTCTCCCTCTCTTACTCTGCTCTCA 87
QY 88 CCATGTGAGACGCTCGCTCCCTCTTGCCTTACACGAGATTGGAAGCTTCTGAGGCC 147
DB 5380 CCATGTGAGATACCT-GCTCCGCTTTGCTTCTACATAGTAAAGCCCTGAGGCC 5438
QY 148 TCCCGAGAAGAGAGCTGCTATGCTTCTGTACAGCTGTAGAGCTATTAGCCAGTTAA 207
DB 5439 TCCCGAGAAGAGAGCTGCTATGCTTCTGTACAGCTGTAGAGCTATTAGCCAGTTAA 5498
QY 208 ACCCATCTCTCATTAATTTCCAGCTCAGGATTTCTTTTGAACAATTGAGATGA 267
DB 5499 ACCCTCTTCTGTATATA-TTACAGCTGTGAGTATCTCTTACAGCAGTGTGAGAACG 5557
QY 268 ACTAATACA 276
DB 5558 ACTAATACA 5566

RESULT 14

US-09-474-699-11
Sequence 11, Application US/09474699
Patent No. 6495130
GENERAL INFORMATION:
APPLICANT: Henderson, Daniel R.
APPLICANT: Yu, De Chao
TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
TITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE THEREOF
FILE REFERENCE: 348022001300
CURRENT APPLICATION NUMBER: US/09/474,699
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/114,262
FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 12047
TYPE: DNA
ORGANISM: Homo Sapien
US-09-474-699-11

Query Match 5.0%; Score 132.2; DB 4; Length 12047;
Best Local Similarity 75.9%; Pred. No. 6.2e-27;
Matches 189; Conservative 0; Mismatches 58; Indels 2; Gaps 2;

QY 28 TGAATCTAGTGTGTTAAAGGCTGAGACCTCTCCCTCTCTTACTCTGCTCTCA 87
DB 5320 TGAATCTAGTGTGTTAAAGGCTGAGACCTCTCCCTCTCTTACTCTGCTCTCA 87
QY 88 CCATGTGAGACGCTCGCTCCCTCTTGCCTTACACGAGATTGGAAGCTTCTGAGGCC 147
DB 5380 CCATGTGAGATACCT-GCTCCGCTTTGCTTCTACATAGTAAAGCCCTGAGGCC 5438
QY 148 TCCCGAGAAGAGAGCTGCTATGCTTCTGTACAGCTGTAGAGCTATTAGCCAGTTAA 207
DB 5439 TCCCGAGAAGAGAGCTGCTATGCTTCTGTACAGCTGTAGAGCTATTAGCCAGTTAA 5498
QY 208 ACCCATCTCTCATTAATTTCCAGCTCAGGATTTCTTTTGAACAATTGAGATGA 267
DB 5499 ACCCTCTTCTGTATATA-TTACAGCTGTGAGTATCTCTTACAGCAGTGTGAGAACG 5557
QY 268 ACTAATACA 276
DB 5558 ACTAATACA 5566

Db 5439 TCCCGAAGCAGATGCCACCATGCTTCTGTACAGCTGACAGAACCATCAGCCAAATTAA 5498
QY 208 ACCCATTTCTTCAATTAATTTCCAGATCTCAGGATATTTCTTTAGCAATTTGAGATGA 267
Db 5499 ACCTCTTTCTGTATTA-TTACCAAGCTTGAGATCTTTACAGCAGTGTGAAACGG 5557
QY 268 ACTAATACA 276
Db 5558 ACTAATACA 5566

RESULT 15

US-09-151-376-3
; Sequence 3, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, B.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 34802200221
; CURRENT APPLICATION NUMBER: US/09/151,376
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-151-376-3

Query Match 5.0%; Score 132.2; DB 4; Length 12047;
Best Local Similarity 75.9%; Pred. No. 6.2e-27;
Matches 189; Conservative 0; Mismatches 58; Indels 2; Gaps 2;

QY 28 TGAATCTAGTTGTTTAAAGCGTGTAGACCTCCCTCTCTTCTTACTCTGCTCTCA 87
Db 5320 TGAGATCTGTCAATTAAAGTGTGTGCCCCCTCCCTCTCTTGTGTCCTACTG 5379
QY 88 CCATGTGAGAGCGCTCGCTCCCTTTGCTTTCACCAAGATTTGAAGCTTCTGAGGCC 147
Db 5380 CCATGTAGATACCT-GCTCTGCTTTGCTTCTTACCATAGTAAAGCCCCCTGAGGCC 5438
QY 148 TCCCGAAGCAGAGCTGCTATGCTTCTGTACAGTCTGTAGAGCTATTAGCCAGTTAA 207
Db 5439 TCCCGAAGCAGATGCACCATGCTTCTGTACAGCTGTGAGCATCAGCCAAATTAA 5498
QY 208 ACCCATTTCTTCAATTAATTTCCAGATCTCAGGATATTTCTTTAGCAATTTGAGATGA 267
Db 5499 ACCTCTTTCTGTATTA-TTACCAAGCTTGAGATCTTTTACAGCAGTGTGAAACGG 5557
QY 268 ACTAATACA 276
Db 5558 ACTAATACA 5566

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OM nucleic - nucleic search, using sw model

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Title: US-09-867-570-1

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Scoring table: IDENTITY_NTC
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Searched: 3413475 seqs, 256380928 residues

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SUMMARIES

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1	2618	100.0	2618	11	US-09-867-570-1
2	1529.6	58.4	1997	14	US-10-219-834-7
3	1483.8	56.7	2040	14	US-10-183-116-15
4	1192.6	45.6	1369	15	US-10-292-798-1273
5	1104	42.2	8622	11	US-09-867-570-3
6	1094.2	41.8	1400	14	US-10-183-116-30
7	1094.2	41.8	1400	15	US-10-225-567A-673
8	1053	40.2	1370	15	US-10-017-161-1599
9	1040.6	39.7	1369	15	US-10-017-161-1055
10	1040.6	39.7	1369	15	US-10-292-798-897
11	1013.6	38.7	1604	14	US-10-183-116-32
12	1013.6	38.7	1604	15	US-10-225-567A-688

13	1012.2	38.7	1369	15	US-10-292-798-1041	Sequence 1041, Ap
14	969	37.0	969	9	US-09-995-225-19	Sequence 19, Appl
15	969	37.0	969	10	US-09-995-225-19	Sequence 19, Appl
16	965.8	36.9	969	15	US-10-401-397A-1	Sequence 1, Appl
17	964.2	36.8	969	15	US-10-391-074-1	Sequence 1, Appl
18	856.2	32.7	997	16	US-10-072-012-111	Sequence 171, App
19	845.8	32.3	909	15	US-10-237-467-9	Sequence 9, Appl
20	833	31.8	969	9	US-09-995-225-17	Sequence 17, Appl
21	833	31.8	969	10	US-09-995-225-17	Sequence 17, Appl
22	833	31.8	969	15	US-10-237-467-3	Sequence 3, Appl
23	829.8	31.7	969	15	US-10-079-384-3	Sequence 3, Appl
24	829.8	31.7	969	15	US-10-240-998-3	Sequence 19, Appl
25	829.8	31.7	969	15	US-10-321-807-19	Sequence 19, Appl
26	829.8	31.7	969	15	US-10-237-467-11	Sequence 43, Appl
27	829.8	31.7	969	15	US-10-343-650A-43	Sequence 19, Appl
28	829.8	31.7	969	17	US-10-321-807-19	Sequence 19, Appl
29	829.8	31.7	969	17	US-10-314-048A-19	Sequence 19, Appl
30	823.2	31.4	1005	16	US-10-072-012-113	Sequence 173, App
31	823.2	31.4	1005	16	US-10-072-012-117	Sequence 177, App
32	792.2	30.3	966	15	US-10-240-998-9	Sequence 9, Appl
33	787.4	30.1	994	16	US-10-072-012-169	Sequence 169, App
34	769.6	29.4	966	15	US-10-240-998-6	Sequence 6, Appl
35	755.4	28.9	769	15	US-10-101-510-239	Sequence 239, App
36	740.2	28.3	955	15	US-10-292-798-1077	Sequence 1077, Ap
37	713.8	27.3	1394	15	US-10-292-798-1269	Sequence 1269, Ap
38	687.8	26.3	955	15	US-10-017-161-1311	Sequence 1311, Ap
39	628.8	24.0	1030	16	US-10-072-012-175	Sequence 175, App
40	618.8	23.6	961	15	US-10-240-998-7	Sequence 7, Appl
41	608.8	23.3	1163	9	US-09-750-373-11	Sequence 11, Appl
42	608.8	23.3	1300	14	US-10-183-116-17	Sequence 11, Appl
43	608.8	23.3	1300	15	US-10-225-567A-648	Sequence 648, App
44	608.8	23.3	1393	15	US-10-017-161-1053	Sequence 1053, Ap
45	608.8	23.3	1393	15	US-10-292-798-895	Sequence 895, App

ALIGNMENTS

RESULT 1
US-09-867-570-1
; Sequence 1, Application US/09867570
; Publication No. US20040076951A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CL000900-CIP
; CURRENT APPLICATION NUMBER: US/09/867,570
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/695,045
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: Human
; US-09-867-570-1

Query Match 100.0%; Score 2618; DB 11; Length 2618;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AACAAATGGCCGCAATTCGCGACGAGATGAATCTAGTTGTTTAAAGCGTGAACCT	60
DB	1	AACAAATGGCCGCAATTCGCGACGAGATGAATCTAGTTGTTTAAAGCGTGAACCT	60
QY	61	CCCTCCCTCTCTCTTACTTCTCTGCTCTCAACATGGAACGCTGCCCTTGGCTTT	120
DB	61	CCCTCCCTCTCTCTTACTTCTCTGCTCTCAACATGGAACGCTGCCCTTGGCTTT	120
QY	121	CACCAAGATGGAAGCTTCTGAGGCTCCCGCAGAAAGCAAGAGCTGTATGTTCTTGA	180

Db	121	CACCGAGATTGGAAGCTTCTGAGGCTCCCGAAGCAGAAAGCTGTAATGCTTTGTA	180
Qy	181	CAGTCTGTAAGACTTATTAGCCAGTTAAACCAATTCCTTCATPAAATTTCCAGTCTCAG	240
Db	181	CAGTCTGTAAGACTTATTAGCCAGTTAAACCAATTCCTTCATPAAATTTCCAGTCTCAG	240
Qy	241	TATTTCTTTTATGCAATTTGAGATGCACTAATPACACAGACAGAGCCAGAGATGGA	300
Db	241	TATTTCTTTTATGCAATTTGAGATGCACTAATPACACAGAGAGCCAGAGATGGA	300
Qy	301	ATCCCAAGTGTCTTCTGCTGCTGCTCAGTCTCCGTGCTGCTGCTCCAGTCTCAAT	360
Db	301	ATCCCAAGTGTCTTCTGCTGCTGCTCAGTCTCCGTGCTGCTGCTCCAGTGTCTCAAT	360
Qy	361	TCACACAGAAACAGAAATPAAAGAAATCCACTGATGATGATACATPAGAAAGCACTCT	420
Db	361	TCACACAGAAACAGAAATPAAAGAAATCCACTGATGATGATACATPAGAAAGCACTCT	420
Qy	421	TGGATGTCAACAGGATPAAAGAAATGAAAAAGCAATCTCTATGAGGTATCAACATG	480
Db	421	TGGATGTCAACAGGATPAAAGAAATGAAAAAGCAATCTCTATGAGGTATCAACATG	480
Qy	481	GATTCTGAGCATGGAATTAACCATCCAGTCTGGGTACAGAACTGACACCAATCAAC	540
Db	481	GATTCTGAGCATGGAATTAACCATCCAGTCTGGGTACAGAACTGACACCAATCAAC	540
Qy	541	GACGTGAGGAGACTCTCTTGCTTCAAGCAGACCCCTGAGCTTCAACGGGCTGACGTGATC	600
Db	541	GACGTGAGGAGACTCTCTTGCTTCAAGCAGACCCCTGAGCTTCAACGGGCTGACGTGATC	600
Qy	601	TTTTCCCTGTGCGCGCTGACAGAAACGGGTTGTGCTCTGCTCCTGCGCTCCGCAATC	660
Db	601	TTTTCCCTGTGCGCGCTGACAGAAACGGGTTGTGCTCTGCTCCTGCGCTCCGCAATC	660
Qy	661	GCAGGAAGCGCTCTCCATCTTACATCTCTCAACCTGATCGAGGCGCACTTCTCTCTTA	720
Db	661	GCAGGAAGCGCTCTCTCCATCTTACATCTCTCAACCTGATCGAGGCGCACTTCTCTCTTA	720
Qy	721	GCGGCGACATTATATGTTGCGCGTTACGCGCTCATCAATATCCGCCATCCATCTCCAAA	780
Db	721	GCGGCGACATTATATGTTGCGCGTTACGCGCTCATCAATATCCGCCATCCATCTCCAAA	780
Qy	781	TCCTCAGTCTGTGATGACCTTTTCCCTACTTATAGAGCTTAAAGACTGTAGAGCCATCA	840
Db	781	TCCTCAGTCTGTGATGACCTTTTCCCTACTTATAGAGCTTAAAGACTGTAGAGCCATCA	840
Qy	841	GCACCGAAGCGCTGCCATCTCTGTGGCCCATCTGATACACATGCGCGCGCCCAAGT	900
Db	841	GCACCGAAGCGCTGCCATCTCTGTGGCCCATCTGATACACATGCGCGCGCCCAAGT	900
Qy	901	ACCTGTCAACGGTCAATGATGTGCTGCTGCTGAGGACCTGTCCCTGCTGAGATATCTGG	960
Db	901	ACCTGTCAACGGTCAATGATGTGCTGCTGCTGAGGACCTGTCCCTGCTGAGATATCTGG	960
Qy	961	AGTGAATGTTCTGTGACTTCTGTTTATGATGATGATGATGATGATGATGATGATGATG	1020
Db	961	AGTGAATGTTCTGTGACTTCTGTTTATGATGATGATGATGATGATGATGATGATGATG	1020
Qy	1021	ATTTCAATTAACATCGCGTGGCTGTTTATATGATGATGATGATGATGATGATGATGATG	1080
Db	1021	ATTTCAATTAACATCGCGTGGCTGTTTATATGATGATGATGATGATGATGATGATGATG	1080
Qy	1081	TCCTGCTGGTCAAGATTCCTGTGGAATCCCGGAAGATGCGCTGACACAGCTGTACGTA	1144
Db	1081	TCCTGCTGGTCAAGATTCCTGTGGAATCCCGGAAGATGCGCTGACACAGCTGTACGTA	1144
Qy	1141	CCATCTCTCTCAAGATGCTGATCTTCTCTCTCTGATGATGATGATGATGATGATGATG	1200
Db	1141	CCATCTCTCTCAAGATGCTGATCTTCTCTCTCTGATGATGATGATGATGATGATGATG	1200
Qy	1201	CCCTGTTTTCAGGATCACTGTGATGAAAGCTTATTTTGTATGTGATCTTATGTTT	1260

D	1201	CCGTGTTTCCAGGATCCACCTGGATTGGAAGTCTTAATTTTGCATGTCATCTAAGTT	1260
Q	1261	CCATTTTCCTGTCCGCTCTTAAACGACAGTGCACAACCCATCATTTACTTCTTGTTGGCT	1320
D	1261	CCATTTTCCTGTCCGCTCTTAAACGACAGTGCACAACCCATCATTTACTTCTTGTTGGCT	1320
Q	1321	CCTTAAGCAGCGTCAAAATAGAGGAGAACCTGAAAGCTGTATTCTCACAAGGACTCTGACAG	1380
D	1321	CCTTAAGCAGCGTCAAAATAGAGGAGAACCTGAAAGCTGTATTCTCACAAGGACTCTGACAG	1380
Q	1381	ACACGCTGAGAGTGGATGAAAGTGGAGGTGGCTTCTCAGAGAAACCTGAGCTGTGCG	1440
D	1381	ACAGCGCTGAGAGTGGATGAAAGTGGAGGTGGCTTCTCAGAGAAACCTGAGCTGTGCG	1440
Q	1441	GAGCAGATTGGAGACAGTGAAGAGAACCTCTGCCCCCTGTACAGACAGACTTTGAGAGCA	1500
D	1441	GAGCAGATTGGAGACAGTGAAGAGAACCTCTGCCCCCTGTACAGACAGACTTTGAGAGCA	1500
Q	1501	TGCTGCCCCGTGCACCCCTTGACAAATTATATGCAATTTTCTTAGCCTTGTGCTCAGAAATG	1560
D	1501	TGCTGCCCCGTGCACCCCTTGACAAATTATATGCAATTTTCTTAGCCTTGTGCTCAGAAATG	1560
Q	1561	TCTCAGTGGTCCCTCAAGTCTTCGAAATGATGTTTACTAACCTGACAGTTGCAGTTT	1620
D	1561	TCTCAGTGGTCCCTCAAGTCTTCGAAATGATGTTTACTAACCTGACAGTTGCAGTTT	1620
Q	1621	CACCCATGGAAGACATTAGTCTGACAGTACAGATGTTGGATTCTCTTGATATTAACAAT	1680
D	1621	CACCCATGGAAGACATTAGTCTGACAGTACAGATGTTGGATTCTCTTGATATTAACAAT	1680
Q	1681	ACATTTTCCCGTATCTGTGACAGTACCTTCCCTACTGAAACCTTTCTGCACTTTTC	1740
D	1681	ACATTTTCCCGTATCTGTGACAGTACCTTCCCTACTGAAACCTTTCTGCACTTTTC	1740
Q	1741	ATTGTAAATAAAGAGTTGCTGTCTCCACAACCTTAAACCTTCTTTACTTGTGTTCTTA	1800
D	1741	ATTGTAAATAAAGAGTTGCTGTCTCCACAACCTTAAACCTTCTTTACTTGTGTTCTTA	1800
Q	1801	CCTGATAGTATCAAAAAGAAAGATTCTTATTAATCTGTACAGTATGTTCCCTGAAAA	1860
D	1801	CCTGATAGTATCAAAAAGAAAGATTCTTATTAATCTGTACAGTATGTTCCCTGAAAA	1860
Q	1861	TCAATTTCCCTTTTATATGCTGGAGGCAATTCAGATGTGAAGTCAATTCTTAATAGT	1920
D	1861	TCAATTTCCCTTTTATATGCTGGAGGCAATTCAGATGTGAAGTCAATTCTTAATAGT	1920
Q	1921	GAGTTCTGCTACCTCTTAAATCCATTAATTTCTCAGATATTAAGCAAAATATGACCTTA	1980
D	1921	GAGTTCTGCTACCTCTTAAATCCATTAATTTCTCAGATATTAAGCAAAATATGACCTTA	1980
Q	1981	GAGAGAGATTCTCCCTCATMAAAACAGTCTTAGAAAATGGTTTATGAATAGCCCTCTC	2040
D	1981	GAGAGAGATTCTCCCTCATMAAAACAGTCTTAGAAAATGGTTTATGAATAGCCCTCTC	2040
Q	2041	CTGTCAATTGTTCACAGATGTGTACATGTGTGGCTTGTCTAGTAAAGCAATGTGT	2100
D	2041	CTGTCAATTGTTCACAGATGTGTACATGTGTGGCTTGTCTAGTAAAGCAATGTGT	2100
Q	2101	GCCCCCTCCCTTGAGAACGTGTAAAGTTCTTAATTTAGCTCTTCTCTGACATTAAGAACTAG	2160
D	2101	GCCCCCTCCCTTGAGAACGTGTAAAGTTCTTAATTTAGCTCTTCTCTGACATTAAGAACTAG	2160
Q	2161	TGAGGAGCCTTAATAATATGTCCACACAGTTTCATTTTGGCATTGGAAACCTCAATATG	2220
D	2161	TGAGGAGCCTTAATAATATGTCCACACAGTTTCATTTTGGCATTGGAAACCTCAATATG	2220
Q	2221	ATTTTAAAGTGAATATATCTTGAAAAACATTATATTAATCACTTAAGATTCCTTCAGTT	2280
D	2221	ATTTTAAAGTGAATATATCTTGAAAAACATTATATTAATCACTTAAGATTCCTTCAGTT	2280
Q	2281	GTAGAGAAATCTTCATATCTCCAGGTTTGTATTAATATGTCTGATGTTGTAACCTTCAGT	2340
D	2281	GTAGAGAAATCTTCATATCTCCAGGTTTGTATTAATATGTCTGATGTTGTAACCTTCAGT	2340
Q	2340	GTAGAGAAATCTTCATATCTCCAGGTTTGTATTAATATGTCTGATGTTGTAACCTTCAGT	2400
D	2340	GTAGAGAAATCTTCATATCTCCAGGTTTGTATTAATATGTCTGATGTTGTAACCTTCAGT	2400

Db 1453 TCGTTCACAAACCTTAAACTCTTCTTATCTGTTGTTCTTACCTGATGATCAAAA 1512
Qy 1818 GGAAGATTCCTTATTAATCTGTCAAGATATGTCCTCCGTAATATCATGTTCCCTTTATG 1877
Db 1513 GGAAGATTCCTTATTAATCTGTCAAGATATGTCCTCCGTAATATCATGTTCCCTTTATG 1572
Qy 1878 ACTGAGGCAATTAAGTGAAGTGAAGTCAATCTTAAATAGTGAATCTGCTA 1937
Db 1573 ACTGAGGCAATTAAGTGAAGTGAAGTCAATCTTAAATAGTGAATCTGCTA 1632
Qy 1938 AATTCATTAATCTGATGATTAAGCAAAATATAGCCTTAAGAGAGATTCCTCCCTT 1997
Db 1633 AATTCATTAATCTGATGATTAAGCAAAATATAGCCTTAAGAGAGATTCCTCCCTT 1692
Qy 1998 CATAAAAAGCTTTAGAAATGTTTATTAATAGATAGCCCTCTGCTATTTGTCACAG 2057
Db 1693 CATAAAAAGCTTTAGAAATGTTTATTAATAGATAGCCCTCTGCTATTTGTCACAG 1752
Qy 2058 CATGATGACATGTTGGCTTGTGTTCTAGTAAGCAATGCTGCTCCCTTCCCTTGAGA 2117
Db 1753 CATGATGACATGTTGGCTTGTGTTCTAGTAAGCAATGCTGCTCCCTTCCCTTGAGA 1812
Qy 2118 ACTGATGATGTTTATTAATAGTCTTCTGCTGATAGCACTAGTGAAGAGGCTATTAATA 2177
Db 1813 ACTGATGATGTTTATTAATAGTCTTCTGCTGATAGCACTAGTGAAGAGGCTATTAATA 1872
Qy 2178 TGTCCCAACAGTTTATTTGGCCATTTGGCAATGAAACCTCATATGATTTTAAAGTGAAT 2237
Db 1873 TGTCCCAACAGTTTATTTGGCCATTTGGCAATGAAACCTCATATGATTTTAAAGTGAAT 1932
Qy 2238 ATCTT--GAAAACCATTTATTTATCACTTACAGA 2269
Db 1933 ATCTTGTGTTTTCATTTATTTATTTACAGGAAGA 1966

RESULT 3
US-10-183-116-15
Sequence 15, Application US/10183116
Publication No. US20030092035A1
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhang
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE ACICP1
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (328)...(1293)
US-10-183-116-15

Query Match 56.7%; Score 1483.8; DB 14; Length 2040;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 1596; Conservative 0; Mismatches 147; Indels 4; Gaps 2;

Qy 462 TCATGGGTCATCAGACTGGGGTTTCTGAGCATGATTCAAACATCCAGTCTTGGGTAC 521
Db 298 TCAGGGTCACAGACTGAGGTTTCTGAGCATGATTCAAACATCCAGTCTTGGGTAC 357
Qy 522 GAATGACACCAATCAACGAGACGTGAGAGACCTCTTGCTGAAAGAGACCCGAGCTTC 581
Db 358 GAATGACACCAATCAACGAGACGTGAGAGACCTCTTGCTGAAAGAGACCCGAGCTTC 417
Qy 582 ACGGGCTGACGTGACGTGTTTCCCTTGTGCGCTGACAGAAACCGGTGTGCTCTG 641
Db 418 ACGGTCTGACGTGACGTGTTTCCCTTGTGCGCTGACAGAAACCGGTGTGCTCTG 477
Qy 642 CTCCTGGGCTGCGCATGCGCAGAGAACGCTGTCTCAATCAATCTTCAACCTGTGCGG 701
Db 478 CTCCTGGGCTGCGCATGCGCAGAGAACGCTGTCTCAATCAATCTTCAACCTGTGCGG 537
Qy 702 GCCATCTTCTCTTCTTACGCGCACAATTATATGTCGCGCTTAAGCCCTCAATATAC 761
Db 538 GCAACCTTCTCTTCTTACGCGCACAATTATATGTCGCGCTTAAAGCTTCAATCAATAT 597
Qy 762 CGCATCCCATCTTCAAAATCTCAGTCTGTATGACCTTTCCTTATATAGGCTTA 821
Db 598 CCCATACCATCTTCAAAATCTCAGTCTGTATGACCTTTCCTTATATAGGCTTA 657
Qy 822 AGCATGCTGACGCGCATCAGCACCGAGCGCTGCTGTCAATCTGTGCGCATCTGATAC 881
Db 658 AGCTTCTGAGTGCCTGAGCACCGAGCGCTGCTGTCAATCTGTGCGCATCTGATAC 717
Qy 882 CACTGCGCGCGCGCGCAATACCTGTATGATGATGATGATGATGATGATGATGATGATG 941
Db 718 CCGTGCACCGCGCGCGCAATACCTGTATGATGATGATGATGATGATGATGATGATG 777
Qy 942 CTGCTGCGAGATATCTGAGTGAATGTTCTGTGATCTTCTGTTAGTGTGCTGATTC 1001
Db 778 CTGCTGCGAGATATCTGAGTGAATGTTCTGTGATCTTCTGTTAGTGTGCTGATTC 837
Qy 1002 GTTGTGTGAACGTGATTCATTTATTAATGCGTGTGATTTTATGTTGTT 1061
Db 838 GCTTGTGTGAACGTGATTCATTTATTAATGCGTGTGATTTTATGTTGTT 897
Qy 1062 CTCTGTGGTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
Db 898 CTCTGTGGTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
Qy 1122 CTGACAGGCTGATGATGATCTCTCTCAAGTGTGCTCTCTCTCTCTCTCTCTCTCT 1181
Db 958 CTGACAGGCTGATGATGATCTCTCTCAAGTGTGCTCTCTCTCTCTCTCTCTCTCT 1017
Qy 1182 CCTTGTGGCATTCAGTGGGCTGTGTTTCCAGATTCACCTGTGATTTGAAAGTCTTAT 1241
Db 1018 CCTTGTGGCATTCAGTGGGCTGTGTTTCCAGATTCACCTGTGATTTGAAAGTCTTAT 1077
Qy 1242 TGTATATGATCTAGTTTCAATTTTCCGTCTTAAACAGAGTGCACACCCATC 1301
Db 1078 TGTATATGATCTAGTTTCAATTTTCCGTCTTAAACAGAGTGCACACCCATC 1137
Qy 1302 ATTACTTCTTCTGAGGCTCTTTAAGGACGTCAAATATAGGAGAACCTGAGTGT 1361
Db 1138 ATTACTTCTTCTGAGGCTCTTTAAGGACGTCAAATATAGGAGAACCTGAGTGT 1197
Qy 1362 CTCAGAGGCTCTGACAGACAGCTGAGGTGATGAGGTGAGAGGCTGCTCTCAG 1421
Db 1198 CTCAGAGGCTCTGACAGACAGCTGAGGTGATGAGGTGAGAGGCTGCTCTCAG 1257
Qy 1422 GAAACCTGAGAGCTGTGGGAGAGCAATTTGAGACAGTGAAGAGAACCTTGGCTGTGA 1481
Db 1258 GAAATCTGAGAGCTGTGGGAGAGCAATTTGAGACAGTGAAGAGAACCTTGGCTGTGA 1317
Qy 1482 GACAGACTTGAAGAGATGCTGCTGACACCTTGAACATTTATATGATTTTCTTA 1541
Db 1318 GACAGACTTGAAGAGATGCTGCTGACACCTTGAACATTTATATGATTTTCTTA 1377

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QY 1542 GCCTTCGCTCAGAAATGCTCAGTGGTCCCTCAAGGCTTCGAAATGATGTTATCTA 1601
DB 1378 GCCTTCGCTCAGAAATGCTCAGTGGTCCCTCAAGGCTTCGAAATGATGTTATCTA 1437
QY 1602 ACCTGACATGTCAGATTTTCAACCATGGAAGAGATTAGTGCAGTACAAATTTGGAT 1661
DB 1438 ACCTGACATGTCAGATTTTCAACCATGGAAGAGATTAGTGCAGTACAAATTTGGAT 1497
QY 1662 TCTCCTGATATATACCAATATCATTTTCCCTGTTATCTTGACATGGAATCTTCTACTGAA 1721
DB 1498 TCTCCTGATATATACCAATATCATTTTCCCTGTTATCTTGACATGGAATCTTCTACTGAA 1557
QY 1722 CACTTTTTCGACATTTTCTTGTATATTAAGAGAGTTCCGTACAAACCTTAACAC- 1616
DB 1558 CACTTTTTCGACATTTTCTTGTATATTAAGAGAGTTCCGTACAAACCTTAACAC- 1616
QY 1782 TCTTTATCTGTTGTTTCCCTACCTGATATCAAAAAGAAAGATTCTTATTAATCTGTCA 1841
DB 1617 TCTTTATCTGTTGTTTCCCTACCTGATATCAAAAAGAAAGATTCTTATTAATCTGTCA 1676
QY 1842 GACTATGTTCCCTGAAATCATGTTCCCTTTATGACTGAGGACATTACTGAGTTGGA 1901
DB 1677 GACTATGTTCCCTGAAATCATGTTCCCTTTATGACTGAGGACATTACTGAGTTGGA 1736
QY 1902 AGCTCAATCTTATATAGTATGAGTTCGTACTACTTAATTCATGATTCAGATATA 1961
DB 1737 AGCTCAATCTTATATAGTATGAGTTCGTACTACTTAATTCATGATTCAGATATA 1796
QY 1962 AAGCAAAATATGACCTTAGAGAGAGATTCCCTTCATATAAAACAGTCTTAGAAATTGG 2021
DB 1797 AAGCAAAATATGACCTTAGAGAGAGATTCCCTTCATATAAAACAGTCTTAGAAATTGG 1856
QY 2022 TTTTAAATGATGAGCTCTCTCTGTCATTTGTCACAGATGATGACATGTTGGCTGGTT 2081
DB 1857 TTTTAAATGATGAGCTCTCTCTGTCATTTGTCACAGATGATGATGTTGGCTGGTT 1916
QY 2082 TCTAGTAAAGACATGTCGCCCCCTTCCCTTGAGAACTGTAAGTCTTATTTAGCTCT 2141
DB 1917 TCTAGTAAAGACATGTCGCCCCCTTCCCTTGAGAACTTTAAGTCTTATTTAGCTCT 1976
QY 2142 TCTGACATATGACATGATGAGAGGCTTAAATATGTCACACAGTTTCATTTGGCC 2201
DB 1977 TCTGACATATGACATGATGAGAGGCTTAAATATGTCACACAGTTTCATTTGGCC 2033
QY 2202 ATTGGA 2208
DB 2034 ATTGGA 2040

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; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1369)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1169)
US-10-292-798-1273

Query Match 45.6%; Score 1192.6; DB 15; Length 1369;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 462 TCATGGATCATGACATGAGGATTTCTGACATGATTAACCAATCCAGTCTTGGTACA 521
DB 171 TCAGGGATCATGACATGAGGATTTCTGACATGATTAACCAATCCAGTCTTGGTACA 220
QY 522 GAATGACACCAATCAACGAGCTGAGAGACTCTTCTGCTAACAGACACCTGAGCTTC 561
DB 231 GAATGACACCAATCAACGAGCTGAGAGACTCTTCTGCTAACAGACACCTGAGCTTC 290
QY 582 AGGGGCTGACGTCATGCTTTCCCTTGTGAGGCTGACAGAAACGGTGTGCTGCG 641
DB 291 AGGGGCTGACGTCATGCTTTCCCTTGTGAGGCTGACAGAAACGGTGTGCTGCG 350
QY 642 CTCCTGGGCTGCGCATGCGCAGAAAGGCTGTCTCATCTACATCTCAACCTGATCGG 701
DB 351 CTCCTGGGCTGCGCATGCGCAGAAAGGCTGTCTCATCTACATCTCAACCTGATCGG 410
QY 702 GCCGACTTCTCTCTTCTTACGGGCCCATTAATGTTGCGCGTTACGCTCATCAATATC 761
DB 411 GCCGACTTCTCTCTTCTTACGGGCCCATTAATGTTGCGCGTTACGCTCATCAATATC 470
QY 762 CGGCATCCCATCCCAAAATCCCTAGTCCGTGATGACCTTTCCCTTATATAGGCTTA 821
DB 471 CGGCATCCCATCCCAAAATCCCTAGTCCGTGATGACCTTTCCCTTATATAGGCTTA 530
QY 822 AGCATGCTAGGCGCATGACACGAGCGCTGCTGTCATCTGAGGCGCATCTGATAC 881
DB 531 AGCATGCTAGGCGCATGACACGAGCGCTGCTGTCATCTGAGGCGCATCTGATAC 590
QY 882 CACTGCGCGCGCCCATGATCTGTGATGATGATGATGATGATGATGATGATGATGATG 941
DB 591 CACTGCGCGCGCCCATGATCTGTGATGATGATGATGATGATGATGATGATGATGATG 650
QY 942 CTGCTGCGGAGATGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATG 1001
DB 651 CTGCTGCGGAGATGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATG 710
QY 1002 GTTGGTGTGAAACGTCAGATTCATTACATGCGCTGCTGCTTCTTATATGATG 1061
DB 711 GTTGGTGTGAAACGTCAGATTCATTACATGCGCTGCTGCTTCTTATATGATG 770
QY 1062 CTCTGTGAGTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
DB 771 CTCTGTGAGTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
QY 1122 CTGACAGGCTGTGACATGACATCTCTCTCAAGTGTGCTGCTGCTGCTGCTGCTG 1181
DB 831 CTGACAGGCTGTGACATGACATCTCTCTCAAGTGTGCTGCTGCTGCTGCTGCTG 890
QY 1182 CCTTGGATTCAGTGGGCGCTGTTTCCAGATCACCTGATGGAAGTCTTATTT 1241
DB 891 CCTTGGATTCAGTGGGCGCTGTTTCCAGATCACCTGATGGAAGTCTTATTT 950
QY 1242 TGTGATGTCATGATGTTTCCATTTTCTGCTGCTGCTTAAACAGCAGTCCATC 1301
DB 951 TGTGATGTCATGATGTTTCCATTTTCTGCTGCTGCTTAAACAGCAGTCCATC 1010
QY 1302 ATTTACTTCTGCTGCTGCTGCTTAAAGAGGCTTAAAGAGGCTTAAAGAGGCTT 1361
DB 1011 ATTTACTTCTGCTGCTGCTTAAAGAGGCTTAAAGAGGCTTAAAGAGGCTT 1070
QY 1362 CTCAGAGGCTCTGAGAGACAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1421

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Db 1071 CTCGAGGGGCTGCGAGGAGACGCTGAGGTGAGGTGGGTGCTTCCTAG 1130
Qy 1422 GAAACCTGAGCTGTGGGAGAGATTGGAGCAGTGAAGAAACCTGCTGCTCA 1481
Db 1131 GAAACCTGAGCTGTGGGAGAGATTGGAGCAGTGAAGAAACCTGCTGCTCA 1190
Qy 1482 GACAGACCTTTGAGAGCAATGCTGCTGCAACCTTGAACAATTATGATTTTCTTA 1541
Db 1191 GACAGACCTTTGAGAGCAATGCTGCTGCAACCTTGAACAATTATGATTTTCTTA 1250
Qy 1542 GCCTTGGCTTCAGAAATGCTGCTGCTGCAAGCTTTCGAATGATTTTCTTA 1601
Db 1251 GCCTTGGCTTCAGAAATGCTGCTGCTGCAAGCTTTCGAATGATTTTCTTA 1310
Qy 1602 ACCTGACAGTTGAGTTTCAACCAAGAAAGATTAGTGAAGTAAATGTTTGA 1660
Db 1311 ACCTGACAGTTGAGTTTCAACCAAGAAAGATTAGTGAAGTAAATGTTTGA 1369

RESULT 5
US-09-867-570-3
; Sequence 3, Application US/09867570
; Publication No. US20040076951A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C0000900-CIP
; CURRENT APPLICATION NUMBER: US/09/867,570
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/695,045
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8622
; TYPE: DNA
; ORGANISM: Human
US-09-867-570-3

Query Match 42.2%; Score 1104; DB 11; Length 8622;
Best Local Similarity 99.6%; Pred. No. 1.9e-300;
Matches 1107; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 462 TCATGGGTCACTGAGGCTTCTGAGCATGATGCAACCTGCTGCTGCTGCTCA 521
Db 7498 TCGAGGGTCACTGAGGCTTCTGAGCATGATGCAACCTGCTGCTGCTCA 7557
Qy 522 GAACTGACCAATCAACGAGCTGAGGAGACTCTCTGCTCAAGCAGACCTGAGCTTC 581
Db 7558 GAACTGACCAATCAACGAGCTGAGGAGACTCTCTGCTCAAGCAGACCTGAGCTTC 7617
Qy 582 ACGGGGCTGACGTGATGCTTTCCCTTGTGGGCTGACAGAAACGCGTTGTGCTGCG 641
Db 7618 ACGGGGCTGACGTGATGCTTTCCCTTGTGGGCTGACAGAAACGCGTTGTGCTGCG 7677
Qy 642 CTCCTGGGCTGCGGAGCGAGAGAGCTGTCTCCATCTCACTCACTCACTGCTGCGG 701
Db 7678 CTCCTGGGCTGCGGAGCGAGAGAGCTGTCTCCATCTCACTCACTCACTGCTGCGG 7737
Qy 702 GCGCACTTCTCTCTTCTTAGCGGCACTATATGTTGCGCGTTAGCGCTCATCAATATC 761
Db 7738 GCGCACTTCTCTCTTCTTAGCGGCACTATATGTTGCGCGTTAGCGCTCATCAATATC 7797
Qy 762 GCGCATCCCATTCGAAAATCTCACTCTGTGATGACCTTTCCTACTTATAGGCTTA 821
Db 7798 GCGCATCCCATTCGAAAATCTCACTCTGTGATGACCTTTCCTACTTATAGGCTTA 7857
Qy 822 AGCATGTGAGCGGAGCATGAGACGAGGCGTCCCTGTCATCTGTGCGCATCTGATAC 881
Db 7858 AGCATGTGAGCGGAGCATGAGACGAGGCGTCCCTGTCATCTGTGCGCATCTGATAC 7917

Qy 882 CACTGCGCGCCGCCAGATACCTGTCAATGCTGATGTGCTCTGCTGCTGCTGCTC 941
Db 7918 CACTGCGCGCCGCCAGATACCTGTCAATGCTGATGTGCTCTGCTGCTGCTGCTC 7977
Qy 942 CTGCTGCGGAGTATCTGAGATGAGATGTTCTGCTGCACTTCTGTTTGTGCTGCTATCT 1001
Db 7978 CTGCTGCGGAGTATCTGAGATGAGATGTTCTGCTGCACTTCTGTTTGTGCTGCTATCT 8037
Qy 1002 GTTTGTGTGAAAGTGAATTCATTAACAATCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1061
Db 8038 GTTTGTGTGAAAGTGAATTCATTAACAATCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8097
Qy 1062 CTCTGTGGGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1121
Db 8098 CTCTGTGGGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8157
Qy 1122 CTGACAGGCTGTACGAGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181
Db 8158 CTGACAGGCTGTACGAGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8217
Qy 1182 CCTTTGGCATTCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1241
Db 8218 CCTTTGGCATTCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8277
Qy 1242 TGTCAATGCAATGATTTTCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
Db 8278 TGTCAATGCAATGATTTTCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8337
Qy 1302 ATTACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1361
Db 8338 ATTACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8397
Qy 1362 CTCGAGAGGCTCTGCAAGACAGCTGAGTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGA 1421
Db 8398 CTCGAGAGGCTCTGCAAGACAGCTGAGTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGA 8457
Qy 1422 GAAACCTGAGCTGTGCGGAGAGCAATGAGAGAGTGAAGAGAACTCTGCTGCTGCTCA 1481
Db 8458 GAAACCTGAGCTGTGCGGAGAGCAATGAGAGAGTGAAGAGAACTCTGCTGCTGCTCA 8517
Qy 1482 GACAGACCTTTGAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
Db 8518 GACAGACCTTTGAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8577
Qy 1542 GCCTTGTGCTCAGAAATGCTCAGTGTGCTC 1573
Db 8578 GCCTTGTGCTCAGAAATGCTCAGTGTGCTC 8609

RESULT 6
US-10-183-116-30
; Sequence 30, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE-4C1CPI
; CURRENT APPLICATION NUMBER: US/10/183,116
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869

PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (332) ... (1297)
US-10-183-116-30

Query Match 41.8%; Score 1094.2; DB 14; Length 1400;
Best Local Similarity 99.7%; Pred. No. 3.4e-298;
Matches 1096; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 462 TCATGGGTCATCAGACTGGGGTTTCTGAGCAGTGAATTCACATCCAGTCTTGGGTACA 521
DB 302 TCAGGGGTACACAGACTGGGGTTTCTGAGCAGTGAATTCACATCCAGTCTTGGGTACA 361
QY 522 GAACGTACACCAATCAACGAGAGTGAAGTCTCTGCTCAACAGAGACCCGTGAGCTTC 581
DB 362 GAACGTACACCAATCAACGAGAGTGAAGTCTCTGCTCAACAGAGACCCGTGAGCTTC 421
QY 582 ACAGGGGTGACAGTCACTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641
DB 422 ACAGGGGTGACAGTCACTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
QY 642 CTCCTGGGCTGCGGATGCGGAGAAAGCTGTCTCATCTACATCTCAACCTGTGCGG 701
DB 482 CTCCTGGGCTGCGGATGCGGAGAAAGCTGTCTCATCTACATCTCAACCTGTGCGG 541
QY 702 GCGCACTTCTCTCTTCTGAGCGGCTCATATATGTTGCGGCTTACGCTCATCATATC 761
DB 542 GCGCACTTCTCTCTTCTGAGCGGCTCATATATGTTGCGGCTTACGCTCATCATATC 601
QY 762 CCGCATCCCATCTCCAAATCTCAGTCTGATGATGATGATGATGATGATGATGATGATG 821
DB 602 CCGCATCCCATCTCCAAATCTCAGTCTGATGATGATGATGATGATGATGATGATGATG 661
QY 822 AGCATGCTGAGCGCATCAACGAGAGTGAAGTCTCTGCTCAACAGAGACCCGTGAGCTTC 881
DB 662 AGCATGCTGAGCGCATCAACGAGAGTGAAGTCTCTGCTCAACAGAGACCCGTGAGCTTC 721
QY 882 CACTGCG 941
DB 722 CACTGCG 781
QY 942 CTGCTGCGAGATCTCTGAGTGAATGTTCTGATCTTCTGTTTGTGAGTCTGATCTT 1001
DB 782 CTGCTGCGAGATCTCTGAGTGAATGTTCTGATCTTCTGTTTGTGAGTCTGATCTT 841
QY 1002 GTTGTGTGAAACGTCAATTTCAATTAACATGCGTGTGTTTGTGAGTCTGATCTT 1061
DB 842 GTTGTGTGAAACGTCAATTTCAATTAACATGCGTGTGTTTGTGAGTCTGATCTT 901
QY 1062 CTCTGTGGGTGCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
DB 902 CTCTGTGGGTGCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 961
QY 1122 CTGACACGAGCTGACGATCTCTGACAGTGTGATCTTCTCTCTCTGAGCTG 1181
DB 962 CTGACACGAGCTGACGATCTCTGACAGTGTGATCTTCTCTCTCTGAGCTG 1021
QY 1182 CCGTTTGGGATTCAGTGGGCTGTTTTCAGAGTCAACCTGTGATGAAAGTCTTAATTT 1241
DB 1022 CCGTTTGGGATTCAGTGGGCTGTTTTCAGAGTCAACCTGTGATGAAAGTCTTAATTT 1081
QY 1242 TGTCAATGTGATCTTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1301
DB 1082 TGTCAATGTGATCTTAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1141
QY 1302 ATTACTTCTGTTGGGCTCTTTAGAGAGCTCAAAATAGAGAGAACTGAAAGTGTGTT 1361

DB 1142 ATTACTTCTGTTGGGCTCTTTAGAGAGCTCAAAATAGAGAGAACTGAAAGTGTGTT 1201
QY 1362 CTCACAGAGGCTTGAAGACAGCTGAGTGTGATGAAAGTGTGAGTGTGCTTCCCTGAG 1421
DB 1202 CTCACAGAGGCTTGAAGACAGCTGAGTGTGATGAAAGTGTGAGTGTGCTTCCCTGAG 1261
QY 1422 GAAACCTGAGCTGTGAGGAGACAGATGAGACAGTGAAGAGAACTCTGCTGCTGCA 1481
DB 1262 GAAACCTGAGCTGTGAGGAGACAGATGAGACAGTGAAGAGAACTCTGCTGCTGCA 1321
QY 1482 GACAGAGCTTGAAGACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
DB 1322 GACAGAGCTTGAAGACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381
QY 1542 GCTTCTGCTGCTGAGAAATG 1560
DB 1382 GCTTCTGCTGCTGAGAAATG 1400

RESULT 7

US-10-225-567A-673
Sequence 673, Application US/10225567A
Publication No. US2003013798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
TITLE OF INVENTION: ROUGH, CHRISTINE L.
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 673
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-673

Query Match 41.8%; Score 1094.2; DB 15; Length 1400;
Best Local Similarity 99.7%; Pred. No. 3.4e-298;
Matches 1096; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 462 TCATGGGTCATCAGACTGGGGTTTCTGAGCAGTGAATTCACATCCAGTCTTGGGTACA 521
DB 302 TCAGGGGTACACAGACTGGGGTTTCTGAGCAGTGAATTCACATCCAGTCTTGGGTACA 361
QY 522 GAACGTACACCAATCAACGAGAGTGAAGTCTCTGCTCAACAGAGACCCGTGAGCTTC 581
DB 362 GAACGTACACCAATCAACGAGAGTGAAGTCTCTGCTCAACAGAGACCCGTGAGCTTC 421
QY 582 ACAGGGGTGACAGTCACTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641
DB 422 ACAGGGGTGACAGTCACTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
QY 642 CTCCTGGGCTGCGGATGCGGAGAAAGCTGTCTCATCTACATCTCAACCTGTGCGG 701
DB 482 CTCCTGGGCTGCGGATGCGGAGAAAGCTGTCTCATCTACATCTCAACCTGTGCGG 541
QY 702 GCGCACTTCTCTTCTTACGCGGCTCATATATGTTGCGGCTTACGCTCATCAATATC 761
DB 542 GCGCACTTCTCTTCTTACGCGGCTCATATATGTTGCGGCTTACGCTCATCAATATC 601
QY 762 CCGCATCCCATCTCCAAATCTCAGTCTGATGATGATGATGATGATGATGATGATGATGATG 821
DB 602 CCGCATCCCATCTCCAAATCTCAGTCTGATGATGATGATGATGATGATGATGATGATGATG 661
QY 822 AGCATGCTGAGCGCATCAACGAGAGTGAAGTCTCTGCTCAACAGAGACCCGTGAGCTTC 881

Db 662 AGCATGCTGAGGCCATCAGACCGAGCGCTGCTGTCATCTGTGGCCCATCTGGTAC 721
 QY 882 CACTGCCGCGCCCGAGATACCTGTCACTGGTCACTGTGTCTGTGGCCCGCTGTCC 941
 Db 722 CACTGCCGCGCCCGAGATACCTGTCACTGGTCACTGTGTCTGTGGCCCGCTGTCC 781
 QY 942 CTGCTGCGGAGTATCTGTGAGTGAATGTTCTGTGACCTTCTGTGTAGTGTGCTGATCT 1001
 Db 782 CTGCTGCGGAGTATCTGTGAGTGAATGTTCTGTGACCTTCTGTGTAGTGTGCTGATCT 841
 QY 1002 GTTTGGTGTGAAGGTGATGATTTCACTTACATCGCGTGGCTGTTTCTTTTAAAGTGTGTT 1061
 Db 842 GTTTGGTGTGAAGGTGATGATTTCACTTACATCGCGTGGCTGTTTCTTTTAAAGTGTGTT 901
 QY 1062 CTCTGTGGTGTCAAGCTGTGTCTGTGTGTGAGATCTCTGTGATCTCCGGAAGATGCG 1121
 Db 902 CTCTGTGGTGTCAAGCTGTGTCTGTGTGTGAGATCTCTGTGATCTCCGGAAGATGCG 961
 QY 1122 CTGACAGGCTGTACGTGACCAATCTCTCAAGTGTGTCTCTCTCTGTGTGGCTG 1181
 Db 962 CTGACAGGCTGTGTACGTGACCAATCTCTCAAGTGTGTCTCTCTCTGTGTGGCTG 1021
 QY 1182 CCCCTTGGCAATCTGAGTGGGCGCTGTTTCCAGGATCCACCTGGAATTTGGAAGCTTATTT 1241
 Db 1022 CCCCTTGGCAATCTGAGTGGGCGCTGTTTCCAGGATCCACCTGGAATTTGGAAGCTTATTT 1081
 QY 1242 TGTCAATGTGATCTGATTTCCATTTTCTGTCCGCTCTTAAACAGAGTGGCAACCCATC 1301
 Db 1082 TGTCAATGTGATCTGATTTCCATTTTCTGTCCGCTCTTAAACAGAGTGGCAACCCATC 1141
 QY 1302 ATTACTTCTTCTGTGGGCTCTTTAGGCAAGCTCAAAATAGGCAAGCTGAGTGTGTT 1361
 Db 1142 ATTACTTCTTCTGTGGGCTCTTTAGGCAAGCTCAAAATAGGCAAGCTGAGTGTGTT 1201
 QY 1362 CTCGAGAGGCTCTGAGGACGACGCTGAGGTGATGTAAGGTGAGGAGTGTGCTCTGAG 1421
 Db 1202 CTCGAGAGGCTCTGAGGACGACGCTGAGGTGATGTAAGGTGAGGAGTGTGCTCTGAG 1261
 QY 1422 GAAACCTGTGAGCTGTGGGAGGAGATTTGAGAGAGTGAAGAACTGTGCTGTCA 1481
 Db 1262 GAAACCTGTGAGCTGTGGGAGGAGATTTGAGAGAGTGAAGAACTGTGCTGTCA 1321
 QY 1482 GACAGAGCTTTGAGAGCAATGCTGCTGCCACCTTGAATTAATGATTTTCTTA 1541
 Db 1322 GACAGAGCTTTGAGAGCAATGCTGCTGCCACCTTGAATTAATGATTTTCTTA 1381
 QY 1542 GCCTTCGCTCAGAAATG 1560
 Db 1382 GCCTTCGCTCAGAAATG 1400

RESULT 8

US-10-017-161-1599
 ; Sequence 1599, Application US/10017161
 ; Publication No. US20030143688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUMA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: AUBURANT, HIROYUKI
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/0152
 ; CURRENT APPLICATION NUMBER: US/10/017.161
 ; CURRENT FILING DATE: 2002-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001/246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2430
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1599
 ; LENGTH: 1370
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

; NAME/KEY: source
 ; LOCATION: (1) .. (1370)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (201) .. (619)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (996) .. (1170)
 ; US-10-017-161-1599
 Query Match 40.2%; Score 1053; DB 15; Length 1370;
 Best Local Similarity 94.4%; Pred. No. 1.5e-286;
 Matches 1136; Conservative 0; Mismatches 60; Indels 7; Gaps 4;
 QY 462 TCATGGGTCACTAGATGGGGTTCCTGAGCATGATTAACATCCAGTCTGGTACA 521
 Db 171 TCAGGGGTCACTAGATGGGGTTCCTGAGCATGATTAACATCCAGTCTGGTACA 230
 QY 522 GAATGACCAATCAACGAGCTGAGAGACTCTCTTGTCAACAGCAGACCTGAGCTTC 581
 Db 231 GAATGACCAATCAACGAGCTGAGAGACTCTCTTGTCAACAGCAGACCTGAGCTTC 230
 QY 582 ACGGGGCTGAGTGCATGTTTCCCTTGTGCGCGCTGACAGGAAACGGGTTGTGCTGG 641
 Db 291 ACGGGGCTGAGTGCATGTTTCCCTTGTGCGCGCTGACAGGAAACGGGTTGTGCTGG 350
 QY 642 CTCCTGGGCTGCGCATGCGAGAGACGCTGTCTCATCTACATCTCAACCTGTGGCG 701
 Db 351 CTCCTGGGCTGCGCATGCGAGAGACGCTGTCTCATCTACATCTCAACCTGTGGCG 410
 QY 702 GCCGACTTCTCTTCTTAGGGGCACTTAATGTTTGGCGTTAGCCCTCATCAATATC 761
 Db 411 GCCGACTTCTCTTCTTAGGGGCACTTAATGTTTGGCGTTAGCCCTCATCAATATC 470
 QY 762 CGCCATCCCATCTCAAAATCTCATGCTGTGATGACCTTCCCTCACTTATAGGCTTA 821
 Db 471 CGCCATCCCATCTCAAAATCTCATGCTGTGATGACCTTCCCTCACTTATAGGCTTA 530
 QY 822 AGCATGCTGAGCGCATCAGACCGAGCGCTGCTGTCAATCTGTGGCCCATCTGTGAC 881
 Db 531 AGCATGCTGAGCGCATCAGACCGAGCGCTGCTGTCAATCTGTGGCCCATCTGTGAC 590
 QY 882 CACTGCCGCGCCCGAGATACCTGTCAATGCTCATGTGTCTGTCTGTGGCCCTGTCC 941
 Db 591 CACT-CGCGCCCGCCAGATACCTGTCAATGCTCATGTGTCTGTCTGTGGCCCTGTCC 649
 QY 942 CTGCGGAGGATCTGAGTGTGATGTTCTGTGATCTCTGTTTATGAGTGTGATCT 1001
 Db 650 CTGCGGAGGATCTGAGTGTGATGTTCTGTGATCTCTGTTTATGAGTGTGATCT 709
 QY 1002 GTTTGGTGTGAACGTGATTTCAATTAACATCGCGTGTGTTTATGAGTGTGTT 1061
 Db 710 GTTGGTGTGTGAACGTGATTTCAATTAACATCGCGTGTGTTTATGAGTGTGTT 769
 QY 1062 CT---CTGTGGGTCAAGCTGTGTCTGTGTGAGATTTCTGTGTGATCTCCGGAAGATG 1118
 Db 770 CTGTGCGGGGGGTCAAGCTGTGTCTGTGTGAGATTTCTGTGTGATCTCCGGAAGATG 829
 QY 1119 CGGCTGACAGAGCT-GTAACGACCAATCTCTCAAGTGTGTGTTCTCTCTGTGG 1177
 Db 830 CGGCTGACAGAGCTGTAACGACCAATCTCTCAAGTGTGTGTTCTCTCTGTGG 889
 QY 1178 CCGTCCCTTTGGCATAGTGTGGCCCTGTTTCCAGGATCCACCTGATTTGGAAGTCTT 1237
 Db 890 CCGTCCCTTTGGCATAGTGTGGCCCTGTTTCCAGGATCCACCTGATTTGGAAGTCTT 947
 QY 1238 ATTTTGTATGTGATCTAGTTTCAATTTTCTGTCTGTCTTTAACAAGCTGCAACC 1297
 Db 948 ATTTTGTATGTGATCTAGTTTCAATTTTCTGTCTGTCTTTAACAAGCTGCAACC 1007
 QY 1298 CATGATTTACTTCTTGTGGGCTCTTTAGGCAAGCTCAAAATAGGAGAACGTAAGCT 1357
 Db 1008 CATGATTTACTTCTTGTGGGCTCTTTAGGCAAGCTCAAAATAGGAGAACGTAAGCT 1067

QY 1358 GGTTCCTCAGAGGGCTCTGCAAGACAGCCTGAGTGAATGAAGTGAAGGTGGCTTCC 1417
DB 1068 GGTTCCTCAGAGGGCTCTGCAAGACAGCCTGAGTGAATGAAGTGAAGGTGGCTTCC 1127
QY 1418 TCAGAAACCTTGAGAGCTGTGCGAAAGCAGATTGAGCACTGAGAAACCTTCCCT 1477
DB 1128 TCAGAAACCTTGAGAGCTGTGCGAAAGCAGATTGAGCACTGAGAAACCTTCCCT 1187
QY 1478 GTGAGCAGAGCTTTGAGAGCAATGCTGCTCCCTCCACCTTGAATTAATGATTTT 1537
DB 1188 GTGAGCAGAGCTTTGAGAGCAATGCTGCTCCCTCCACCTTGAATTAATGATTTT 1247
QY 1538 CTTAGCTTCTGCTGAGAAATGCTCAGTGTCCCTCAAGTCTTGAATGATTTT 1597
DB 1248 CTTAGCTTCTGCTGAGAAATGCTCAGTGTCCCTCAAGTCTTGAATGATTTT 1307
QY 1598 TCTAACCTGACAGTTGAGTTTCACCATGAAAGATTAGTCTGACAGTACATGTTT 1657
DB 1308 TCTAACCTGACAGTTGAGTTTCACCATGAAAGATTAGTCTGACAGTACATGTTT 1367
QY 1658 GGA 1660
DB 1368 GGA 1370

RESULT 9

US-10-017-161-1055
; Sequence 1055, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SIWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1055
; LENGTH: 1369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1369)
; NAME/KEY: CDS
; LOCATION: (201)..(1169)
US-10-017-161-1055

Query Match 39.7%; Score 1040.6; DB 15; Length 1369;
Best Local Similarity 91.7%; Pred. No. 4.9e-283; Indels 0; Gaps 0;
Matches 1100; Conservative 0; Mismatches 99;

QY 462 TCATGGGTCATCAGACTGGGTTTCTGAGCATGATTCACACATCCAGCTTGGGTACA 521
DB 171 TCAGAGGTCAAGACTGAGGTTTCTGAGCATGATTCACACATCCAGCTTGGGTACA 230
QY 522 GAACTGACACCAATCAACGAGAGCTGAGAGACTTCTTGTCAACAGACCTGAGCTTC 581
DB 231 GAACTGACACCAATCAACGAGAGACTTCTTGTCAACAGACCTGAGCTTC 290
QY 582 ACGGGCTGACGTGACATGCTTCCCTTGTGCGCTGACAGAAACGCGGTGCTCTGG 641
DB 291 ACGGGCTGACGTGACATGCTTCCCTTGTGCGCTGACAGAAACGCGGTGCTCTGG 350
QY 642 CTCCTGGGCTGCGCATGCGCAGGAAGCTGTCTCCATCTCAATCCCACTGCTCGCG 701
DB 642 CTCCTGGGCTGCGCATGCGCAGGAAGCTGTCTCCATCTCAATCCCACTGCTCGCG 701

DB 351 CTCCTGGGCTGCGCATGCGCAGGAAGCTGTCTCCATCTCAATCCCACTGCTCGCGCA 410
QY 702 GCGACTTCTCTCTCTTACGCGCCACATTAATATGTTGCGCGTTAGCCCTCAATCAATATC 761
DB 411 GCGACTTCTCTCTCTTACGCGCGCCCTTAATATATGTTGCGCGCTTCAATCAATATC 470
QY 762 CCGCATCCCATCTCCAAATCTCACTGATCTGTGATGACCTTTCCCTTAATTAAGCTTA 821
DB 471 CCCATACCATCTCTAAATATCTCTATCTGATGATGATTTTCCATCTTGAAGGCTTG 530
QY 822 AGCATCTGAGGCGCATACGACACGAGCGCTGCTGTCAATCTGTGCGCCATCTGTATC 881
DB 531 AGCTTCTGAGGCGCATACGACACGAGCGCTGCTGTGTGCTGTGCGCCATCTGTATC 590
QY 882 CACTGCGCGCGCCGATACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 941
DB 591 CCGTGCACCGCGCCGACACACCTGTACGCGGATGATGATGATGATGATGATGATGATGAT 650
QY 942 CTGCTGCGAGATATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1001
DB 651 CTGCTGCGAGATATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 710
QY 1002 GTTGTGTGAAACGTCAAGATTTCAATTAACATGCGGTGCTGATTTTATATGTGTT 1061
DB 711 GTTGTGTGAAACGTCAAGATTTCAATTAACATGCGGTGCTGATTTTATATGTGTT 770
QY 1062 CTCCTGCGGCTGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1121
DB 771 CTCCTGCGGCTGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
QY 1122 CTGACAGGCTGTACCTGACCAATCTCTCAAGTGTGCTGCTCTCTCTGCTGCTGCTG 1181
DB 831 CTGACAGGCTGTACCTGACCAATCTCTCAAGTGTGCTGCTCTCTCTGCTGCTGCTG 890
QY 1182 CCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1241
DB 891 CCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 950
QY 1242 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1301
DB 951 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1010
QY 1302 ATTTACTTCTGCTGCGGCTCTTTAGCAGCGTCAAAATAGGCAAGCTGAGTGT 1361
DB 1011 ATTTACTTCTGCTGCGGCTCTTTAGCAGCGTCAAAATAGGCAAGCTGAGTGT 1070
QY 1362 CTCAGAGGCTCTGAGAGACAGCTGAGATGAAAGTGAAGGTGGTCTCTCAG 1421
DB 1071 CTCAGAGGCTCTGAGAGACAGCTGAGATGAAAGTGAAGGTGGTCTCTCAG 1130
QY 1422 GAAACCTGAGAGCTGCGGAAAGCAATGAGCAATGAGAGAAACCTGCGCTGTA 1481
DB 1131 GAAACCTGAGAGCTGCGGAAAGCAATGAGCAATGAGAGAAACCTGCGCTGTA 1190
QY 1482 GACAGAGCTTGAAGCAATGCTGCGCTGCAACCTTGAACAATTAATGATTTTCTTA 1541
DB 1191 GACAGAGCTTGAAGCAATGCTGCGCTGCAACCTTGAACAATTAATGATTTTCTTA 1250
QY 1542 GCCTTCTGCTGCAAAATGCTCAAGTGTCTTCAAGGTCTTGAATTAATGATTTTCTTA 1601
DB 1251 GCCTTCTGCTGCAAAATGCTCAAGTGTCTTCAAGGTCTTGAATTAATGATTTTCTTA 1310
QY 1602 ACCTGACATGATGATTTTCAACCAAGAAAGATTAGTCTGACATGATGATTTTGA 1660
DB 1311 ACCTGACATGATGATTTTCAACCAAGAAAGATTAGTCTGACATGATGATTTTGA 1369

RESULT 10

US-10-292-798-897
; Sequence 897, Application US/10292798
; Publication No. US2003023583A1
; GENERAL INFORMATION:
; APPLICANT: SIWA, MAKIKO

Query Match 38.7%; Score 1013.6; DB 14; Length 1604;
Best Local Similarity 91.0%; Pred. No. 2,4e-275;
Matches 1090; Conservative 0; Mismatches 104; Indels 4; Gaps 1;

QY 466 GGGTCATCAGACTGGGGTTTCTGAGCATGGAATTCACATCCAGTCTGGGTACAGAAC 525
DB 407 GGGGCACACAGACTAGAGTTTCTGAGCATGGAATTCACATCCAGTCTGGGTACAAAC 466
QY 526 TGAACCAATCAACGAGCGTGAAGAGACTCTCTGTCTACAGAGAACCCCTGAGCTTACCG 585
DB 467 TGAACCAATCAACGAGCGTGAAGAGACTCTCTGTCTACAGAGAACCCCTGAGCTTACCG 526
QY 586 GGCCTGAGTGCATGCTTCCCTTGTGCGCGCTGACAGGAAACGGGTTGTCTGTGCTCC 645
DB 527 TGCCTGAGTGCATGCTTCCCTTGTGCGCGCTGACAGGAAACGGGTTGTCTGTGCTCC 586
QY 646 TGGGCTGCGCGCATGCGGAGAGACGCTGTCTCATCTACATCTTCACTGTGCGCGCG 705
DB 587 TGGGCTACCGCATGCGGAGAGACGCTGTCTCATCTACATCTTCACTGTGCGCGCGAG 646
QY 706 ACTTCCCTCTCTTAAGGCGGACATATATGTTCGCGTTACGCGTCAATATATCCGCC 765
DB 647 ACTTCCCTCTCTCAAGTTTCAAGTATATATGCTTCCATTAACGCTCATATATACGCC 706
QY 766 ATCCCATCTCCAAATCTCAGTCTGATGATGACCTTCCCTTATATAGGCTTAAGCA 825
DB 707 ATCTCATCCGCAAAATCTCTGTTCTGTGATGACCTTCCCTTATATAGGCTTAAGCA 766
QY 826 TGCCTGAGCGGCATCAGACACCGAGCGCTGCTGTCCATCTGTGCGCGCATGTGACACT 885
DB 767 TGCCTGAGCGGCATCAGACACCGAGCGCTGCTGTCTGTGCTGTGCGCGCATGTGACACT 826
QY 886 GCGCGCGCGCCCAATACCTGTCTCATCTGATGATGATGATGATGATGATGATGATGAT 945
DB 827 GCGCGCGCGCCCAATACCTGTCTCATCTGATGATGATGATGATGATGATGATGATGAT 886
QY 946 TGGGAGATCTCTGAGTGAAGTCTGTGATCTTCTGATGATGATGATGATGATGATGAT 1005
DB 887 TGTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 946
QY 1006 GGTGTGAAACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065
DB 947 GGTGTGAAACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
QY 1066 GTGGGTCACAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1125
DB 1007 GTGTGTCTCAAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1066
QY 1126 CCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1185
DB 1067 CCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1126
QY 1186 TTTGCAATTCAGTGGGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1245
DB 1127 TTTGCAATTCAGTGGGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1186
QY 1246 ATGTGATCTAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1305
DB 1187 ATGTGATCTAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1246
QY 1306 ACTTCT 1365
DB 1247 ACTTCT 1306
QY 1366 AGAGGGCTCTGACAGACACGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1425
DB 1307 AGAGGGCTCTGACAGACACGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1366
QY 1426 CCTGTGAGCTGTGGGGAAGCATTTGAGAGCATGAGAGAACTCTGTGCTCTCTCTCTCT 1481
DB 1367 GCGTGTGAGCTGTGGGGAAGCATTTGAGAGCATGAGAGAACTCTGTGCTCTCTCTCTCT 1426
QY 1482 GACAGGATCTTGAAGAGATGCTGCGCTGCAACCTTGAACATTAATATGATTTTCTTA 1541

DB 1427 GAGGGGACTTTGAGAGCAACACTGCTCTGCAACCTTGAACATTAATATGAGTCTTTCTTA 1486
QY 1542 GCGTTTGGCTCTGGAATGTCTGAGTGTCTCTGAGAGTCTTCTGATATGTTTATCTTA 1601
DB 1487 GCGTTTGGCTCTGGAATGTCTGAGTGTCTCTGAGAGTCTTCTGATATGTTTATCTTA 1546
QY 1602 ACCGTACAGTTCAGTTCATCCCATGGAAGCATTAATGTCAGTACATTAATGTTTGG 1659
DB 1547 ACCGTACAGTTCAGTTCATCCCATGGAAGCATTAATGTCAGTACATTAATGTTTGG 1604

RESULT 12
US-10-225-567A-688
; Sequence 688, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 688
; LENGTH: 1604
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-688

Query Match 38.7%; Score 1013.6; DB 15; Length 1604;
Best Local Similarity 91.0%; Pred. No. 2,4e-275;
Matches 1090; Conservative 0; Mismatches 104; Indels 4; Gaps 1;

QY 466 GGGTCATCAGACTGGGGTTTCTGAGCATGGAATTCACATCCAGTCTGGGTACAGAAC 525
DB 407 GGGGCACACAGACTAGAGTTTCTGAGCATGGAATTCACATCCAGTCTGGGTACAAAC 466
QY 526 TGAACCAATCAACGAGCGTGAAGAGACTCTCTGTCTACAGAGAACCCCTGAGCTTACCG 585
DB 467 TGAACCAATCAACGAGCGTGAAGAGACTCTCTGTCTACAGAGAACCCCTGAGCTTACCG 526
QY 586 GGCCTGAGTGCATGCTTCCCTTGTGCGCGCTGACAGGAAACGGGTTGTCTGTGCTCC 645
DB 527 TGCCTGAGTGCATGCTTCCCTTGTGCGCGCTGACAGGAAACGGGTTGTCTGTGCTCC 586
QY 646 TGGGCTGCGCGCATGCGGAGAGACGCTGTCTCATCTACATCTTCACTGTGCGCGCG 705
DB 587 TGGGCTACCGCATGCGGAGAGACGCTGTCTCATCTACATCTTCACTGTGCGCGCGAG 646
QY 706 ACTTCCCTCTCTTAAGGCGGACATATATGTTCGCGTTACGCGTCAATATATCCGCC 765
DB 647 ACTTCCCTCTCTCAAGTTTCAAGTATATATGCTTCCATTAACGCTCATATATACGCC 706
QY 766 ATCCCATCTCCAAATCTCAGTCTGATGATGACCTTCCCTTATATAGGCTTAAGCA 825
DB 707 ATCTCATCCGCAAAATCTCTGTTCTGTGATGACCTTCCCTTATATAGGCTTAAGCA 766
QY 826 TGCCTGAGCGGCATCAGACACCGAGCGCTGCTGTCTCATCTGTGCGCGCATGTGACACT 885
DB 767 TGCCTGAGCGGCATCAGACACCGAGCGCTGCTGTCTCATCTGTGCGCGCATGTGACACT 826
QY 886 GCGCGCGCGCCCAATACCTGTCTCATCTGATGATGATGATGATGATGATGATGATGAT 945
DB 827 GCGCGCGCGCCCAATACCTGTCTCATCTGATGATGATGATGATGATGATGATGATGAT 886
QY 946 TGGGAGATCTCTGAGTGAAGTCTGTGATCTTCTGATGATGATGATGATGATGATGAT 1005

Db 887 TGTATTAGTCTGAGTGAAGTTCTGTACTTCTCTTTAGTGTGCTGATTTCTAGTT 946
Qy 1006 GGTGTGAACCTGACATTTTCAATTCAGTGTGCTGATTTTATGTTGTTCTCT 1065
Db 947 GGTGTGAACCTGACATTTTCAATTCAGTGTGCTGATTTTATGTTGTTCTCT 1006
Qy 1066 GTGGGTCACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1125
Db 1007 GTGTTTCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1066
Qy 1126 CCAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1185
Db 1067 CCAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1126
Qy 1186 TTGGCATTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1245
Db 1127 TTGGCATTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1186
Qy 1246 ATGTGATTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1305
Db 1187 ATGTGATTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1246
Qy 1306 ACTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1365
Db 1247 ACTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1306
Qy 1366 AGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1425
Db 1307 AGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1366
Qy 1426 CCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1481
Db 1367 CCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1426
Qy 1482 GACGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1541
Db 1427 GACGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1486
Qy 1542 GCTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1601
Db 1487 GCTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1546
Qy 1602 ACCTGACATTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1659
Db 1547 ACCTGACATTCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1604

RESULT 13
US-10-292-798-1041
Sequence 1041, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURAYANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1041
LENGTH: 1369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:

LOCATION: (1)..(1369)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(1169)
US-10-292-798-1041

Query Match 38.7%; Score 1012.2; DB 15; Length 1369;
Best Local Similarity 91.0%; Pred. No. 5.4e-275;
Matches 1088; Conservative 0; Mismatches 103; Indels 4; Gaps 1;

Qy 466 GGTGTGACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 525
Db 175 GGTGTGACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 234
Qy 526 TGACACCAATCAACGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 585
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Qy 586 GGTGTGACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 645
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Qy 646 TGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 705
Db 355 TGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 414
Qy 706 ACTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 765
Db 415 ACTTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 474
Qy 766 ATCCATCTCCAAATCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 825
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Db 715 GGTGTGAAAGCTGATTTTCAATTCAGTGTGCTGTGCTGTGCTGTGCTGTG 774
Qy 1066 GTGGGTCACAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1125
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/ APPLICANT: Chu, Zhi Liang
 / APPLICANT: Dang, Huong T.
 / APPLICANT: Lowitz, Kevin P.
 / APPLICANT: Priddy, Cameron
 / TITLE OF INVENTION: Endogenous And No. US200301358849-Endogenous Versions of Human C
 / TITLE OF INVENTION: Receptors
 / FILE REFERENCE: AREN-0308
 / CURRENT APPLICATION NUMBER: US/09/995,225
 / CURRENT FILING DATE: 2001-11-26
 / PRIOR APPLICATION NUMBER: 09/170,496
 / PRIOR FILING DATE: 1998-10-13
 / PRIOR APPLICATION NUMBER: PCT/US99/23938
 / PRIOR FILING DATE: 1998-10-13
 / PRIOR APPLICATION NUMBER: 60/253,404
 / PRIOR FILING DATE: 2000-11-27
 / PRIOR APPLICATION NUMBER: 60/255,366
 / PRIOR FILING DATE: 2000-12-12
 / PRIOR APPLICATION NUMBER: 60/270,286
 / PRIOR FILING DATE: 2001-02-20
 / PRIOR APPLICATION NUMBER: 60/282,365
 / PRIOR FILING DATE: 2001-04-06
 / PRIOR APPLICATION NUMBER: 60/270,266
 / PRIOR FILING DATE: 2001-02-20
 / PRIOR APPLICATION NUMBER: 60/282,032
 / PRIOR FILING DATE: 2001-04-06
 / PRIOR APPLICATION NUMBER: 60/282,358
 / PRIOR FILING DATE: 2001-04-06
 / PRIOR APPLICATION NUMBER: 60/282,356
 / PRIOR FILING DATE: 2001-04-06
 / PRIOR APPLICATION NUMBER: 60/290,917
 / PRIOR FILING DATE: 2001-05-14
 / PRIOR APPLICATION NUMBER: 60/309,208
 / PRIOR FILING DATE: 2001-07-31
 / NUMBER OF SEQ ID NOS: 67
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 19
 / LENGTH: 969
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: No. US200301358849el Sequence
 / US-09-995-225-19

Query Match 37.0%; Score 969; DB 10; Length 969;
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 Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 121 GCGCTGACAG 180
 QY 672 GTCCTCACTACATCTCAACCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 731
 DB 181 GTCCTCACTACATCTCAACCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 QY 732 ATATGTTGCGGCTACAGGCTCATCAATATCGGCGCATCCCATCCCAAAATCTGAGTCT 791
 DB 241 ATATGTTGCGGCTACAGGCTCATCAATATCGGCGCATCCCATCCCAAAATCTGAGTCT 300
 QY 792 GTGATGACCTTCCCTACTTATAGGCTTAAGCATGTGAGGAGCATGACGACGAGGAG 851
 DB 301 GTGATGACCTTCCCTACTTATAGGCTTAAGCATGTGAGGAGCATGACGACGAGGAG 360
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DB 361 TGCCGTGCATCTGCTGCGCATCTGTGACCATGCGGCGGCGGCGGCGGCGGCGGCGG 420
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 DB 541 ATCCGCGGCGGCTGTTTATATGAGTGTCTGAGGCGGCGGCGGCGGCGGCGGCGGCT 600
 QY 1092 AGAATTCCTGCTGATCCCGAGAGATCCGCTGACAGGCTGTACGTGACCATCTCTC 1151
 DB 601 AGAATTCCTGCTGATCCCGAGAGATCCGCTGACAGGCTGTACGTGACCATCTCTC 660
 QY 1152 ACAAGTCTGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
 DB 661 ACAAGTCTGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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 DB 721 AGAATTCACCTGATGAGAAAGCTTATTTGTGATGATGATGATGATGATGATGATG 780
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 DB 841 CGTCAAAATAGGCAAGAACTGAGAGCTGTTCTCCAGAGAGGCTCTGACAGACAGCTGAG 900
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 DB 901 GTGATGAGAGTGAAGGCTGCTCTCAGAGAAACCTGAGGCTGTCGAGAGACAGATTG 960
 QY 1452 GAGCAGTGA 1460
 DB 961 GAGCAGTGA 969

Search completed: October 29, 2004, 19:12:59
 Job time : 1223 secs

RESULT 1	AX429465	2618 bp	DNA	linear	PAT 21-JUN-2002
LOCUS	AX429465				
DEFINITION	Sequence 1 from Parent MO0234914.				
ACCESSION	AX429465				
VERSION	AX429465.1	GI:21540763			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE					
AUTHORS	1 Zhao, Q., Beasley, E.M. and Wei, M.H.				
TITLE	Isolated human g-protein coupled receptors, nucleic acid molecules				
	encoding human gpcr proteins, and uses thereof				
JOURNAL	Patent: WO 0234914-A 1 02-MAY-2002;				
	PE CORP NY (US)				
FEATURES					
Source	Location/Qualifiers				
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	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
Query Match	100.0%;	Score 2618;	DB 6;	Length 2618;	
Best Local Similarity	100.0%;	Pred. NO. 0;			
Matches 2618;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 AACAAATGCCCGCAATTCGGCAGCAGATGAATCTAGTTGTTTAAAGCGGTAGCACTT	60			
DB	1 AACAAATGCCCGCAATTCGGCAGCAGATGAATCTAGTTGTTTAAAGCGGTAGCACTT	60			
QY	61 CTTCCCTCTCTTAATCTCTGCTCTTCAACATGTAGAGCGCTCGCTCCCTTTGGCCTTT	120			
DB	61 CTTCCCTCTCTTAATCTCTGCTCTTCAACATGTAGAGCGCTCGCTCCCTTTGGCCTTT	120			
QY	121 CACCAAGATTGAAGCTTCCCTGAGCGCTCCCAAGACAGAAAGCTGTATGCTTCTGTA	180			
DB	121 CACCAAGATTGAAGCTTCCCTGAGCGCTCCCAAGACAGAAAGCTGTATGCTTCTGTA	180			
QY	181 CAGTCTGAGACTTATTAGCAGTTAAACCATTTCTTCAATAATTTCCAGTCTCAGG	240			
DB	181 CAGTCTGAGACTTATTAGCAGTTAAACCATTTCTTCAATAATTTCCAGTCTCAGG	240			

Db 181 CAGTCTGATGAGCTATTAGCCAGTTAAACCCATTTCTTCAATAATTTCCAGTCTCAGG 240
Qy 241 TATTTCTTTTATGCAATTTGAGATGAATGAATTAATACAGACAGAGAGAGAGATGAAA 300
Db 241 TATTTCTTTTATGCAATTTGAGATGAATGAATTAATACAGACAGAGAGAGATGAAA 300
Qy 301 ATCCCAAGGTGCTTTCTGCTGTCTTCCAGTCTCTGCTGTGTCTTCCAGTGTCTCAAT 360
Db 301 ATCCCAAGGTGCTTTCTGCTGTCTTCCAGTCTCTGCTGTGTCTTCCAGTGTCTCAAT 360
Qy 361 TCCACCAAAACCAAAATTAATAAGATCCCACTGATGTGTATCATATGAAGCCACTCT 420
Db 361 TCCACCAAAACCAAAATTAATAAGATCCCACTGATGTGTATCATATGAAGCCACTCT 420
Qy 421 TGGGATGTCAAAAGATTAAGAAATGAAAGCAATCTCATAGGTCTATCAGACTG 480
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Qy 481 GGTTCGTAGCAATGATTCACATCCAGTCTTGGGTACAGAACTGACACCAATCAAG 540
Db 481 GGTTCGTAGCAATGATTCACATCCAGTCTTGGGTACAGAACTGACACCAATCAAG 540
Qy 541 GACGTGAGAGAGATCTCTTGTCTACAGAGAGACCTGAGCTTCAAGGGCTGAGCTGATG 600
Db 541 GACGTGAGAGAGATCTCTTGTCTACAGAGAGACCTGAGCTTCAAGGGCTGAGCTGATG 600
Qy 601 TTTCCCTGTGCGCTGACAGAGAAAGCGGTTGTGTCTGTGCTCTGAGGCTGCGCATG 660
Db 601 TTTCCCTGTGCGCTGACAGAGAAAGCGGTTGTGTCTGTGCTCTGAGGCTGCGCATG 660
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Db 661 GCAGAGAGCGTGTCTCCATCTTACATCTTCAACCTGTGTGCGCGGCGGCTTCTCTT 720
Qy 721 GCGGCAATTAATATGTTGCGCGGTTACGCGCTATGAAATCCGCGCATCCCATCTCCAAA 780
Db 721 GCGGCAATTAATATGTTGCGCGGTTACGCGCTATGAAATCCGCGCATCCCATCTCCAAA 780
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Db 781 TCTCATGCTGTGTATGACCTTTCCCTATCTTTATAGGCTTAAGCATGTGAGGCGCAT 840
Qy 841 GCACCGAGCGCTGCTGTCTCATCTGTGTGCGCATCTGTATCACTGCGCGCGCGCAT 900
Db 841 GCACCGAGCGCTGCTGTCTCATCTGTGTGCGCATCTGTATCACTGCGCGCGCGCAT 900
Qy 901 ACCGTATACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 ACCGTATACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 961 AGTGAATGTTCTGTATCTTCTGTATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 AGTGAATGTTCTGTATCTTCTGTATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 1021 ATTTCAATTAACAATGCGGTGCTGTTTTTATATGATGATGATGATGATGATGATGAT 1080
Db 1021 ATTTCAATTAACAATGCGGTGCTGTTTTTATATGATGATGATGATGATGATGATGAT 1080
Qy 1081 TCCGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 TCCGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Qy 1141 CCATCTCTCTCAAGATGCTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Db 1141 CCATCTCTCTCAAGATGCTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Qy 1201 CCGCTGTTTTCAAGATGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
Db 1201 CCGCTGTTTTCAAGATGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
Qy 1261 CCAATTTTCTGTCTGTCT 1320
Db 1261 CCAATTTTCTGTCTGTCT 1320

Qy 1321 CCTTAGGCAAGCGTCAAAAATAGGCAAACTGAGAGCTGTTCTCCAGAGGCTCTGACG 1380
Db 1321 CCTTAGGCAAGCGTCAAAAATAGGCAAACTGAGAGCTGTTCTCCAGAGGCTCTGACG 1380
Qy 1381 ACAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 ACAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy 1441 GAAGAGATTTGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 GAAGAGATTTGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 TGCTGCGCTGCCAGCTTGCATTAATATGATTTTCTTATGCTTGTGCTCAGAAATG 1560
Db 1501 TGCTGCGCTGCCAGCTTGCATTAATATGATTTTCTTATGCTTGTGCTCAGAAATG 1560
Qy 1561 TCTCATGATGCTCTCTCAAGGTCTTCCAAATATGATTTTCTTAACTGACAGATGCT 1620
Db 1561 TCTCATGATGCTCTCTCAAGGTCTTCCAAATATGATTTTCTTAACTGACAGATGCT 1620
Qy 1621 CACCCATGGAAGCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 CACCCATGGAAGCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Qy 1681 ACAATTTTCCCTGTATCTTGCATGATCTTCTCTCTCTCTCTCTCTCTCTCTCT 1740
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Db 1801 CCGATATGATCAAAAAGAGAGATCTTATTAATCTGTCAAGATGATGATGATGATG 1860
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Qy 1921 GAGTTCTGTACTCTTAATTTCAATTTGAATTTCTGATATTAAGAAATTAATGACT 1980
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Qy 1981 GAGAGAGATTTCCCTCTCAATAAAGAGCTTAGAAATTTGTTTATGATGATGATG 2040
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Qy 2101 GCGCCCTTCCCTTGAAGAGCTGATGATTTTATGATGATGATGATGATGATGATGAT 2160
Db 2101 GCGCCCTTCCCTTGAAGAGCTGATGATTTTATGATGATGATGATGATGATGATGAT 2160
Qy 2161 TGAGAGAGCTTAATAATATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
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Qy 2221 ATTTTAAAGTGAATAATATCTTGAATAACATTTATATCACTTACAGATTTCTT 2280
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Qy 2341 TAGTTTATGCTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
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OY	2461	TCTCAATTATGTAATCTGGATAAATACCTAGTTCGTGAACAANTTCGATACAAATCGTG	2466
Dd	2401	TTCTCAATTATGTAATCTGGATAAATACCTAGTTCGTGAACAANTTCGATACAAATCGTG	2466
OY	2461	GACATACATGAACCTGGAATAATTTGTGCTTAGAGAATAATAGCCAGCCCAAACAATATT	2520
Dd	2461	GACATACATGAACCTGGAATAATTTGTGCTTAGAGAATAATAGCCAGCCCAAACAATATT	2520
OY	2511	GTAAGTTCAAATTTCTATGAGGTATCCAAATTTAGGAATTTCTTGAACACAGAAAAATTAATT	2580
Dd	2521	GTAAGTTCAAATTTCTATGAGGTATCCAAATTTAGGAATTTCTTGAACACAGAAAAATTAATT	2580
OY	2581	AGGAGGATCCTGCTGCCTGGAIAAAAAAAAAAAAAAAAAAAAAA	2618
Dd	2581	AGGAGGATCCTGCTGCCTGGAIAAAAAAAAAAAAAAAAAAAAAA	2618

RESULT 2	
AC108007/c	
LOCUS	AC108007 91923 bp DNA linear PRI 03-SEP-2002
DEFINITION	Homo sapiens chromosome 11, clone CTD-3038L12, complete sequence.
ACCESSION	AC108007
VERSION	AC108007.5 GI:22655822
KEYWORDS	HTG.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	Birken,B., Nusbaum,C. and Lander,E.
JOURNAL	Homo sapiens chromosome 11, clone CTD-3038L12
REFERENCE	unpublished
AUTHORS	2 (bases 1 to 91923)
	Birken,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 91923)

Bittern,B., Nisbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barua,N., Baetien,V., Bloom,T., Boguslavskiy,L., Bouthgalter,B., Camarata,J., Chang,J., Chazaro,B., Cook,P., Collymore,A., Cook,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Kanat,A., Karatae,A., Kells,C., Lacroque,K., Lamataes,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Margus,N., Matthews,C., McCarthy,M., McDonald,P., Major,J., Margus,N., Matthews,C., McCarthy,M., Mcwan,P., McKernan,K., Meldrum,J., Menus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Notman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Retta,R., Ribback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliou,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W., Young,G., Zainoun,J., Zemek,L., Zimmer,A. and Zody,M.

Smith,C., Spencer,B., Stange,Thomann,N., Stojanovic,N., Talams,J.,
Teefaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (124-AUG-2002) Whitehead Institute/MIT Center for Genome
Research 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 91923)

Biten,B., Nusbund,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barra,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
Camarata,J., Chang,Y., Chazaro,B., Choquet,Y., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gird,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
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Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (103-SEP-2002) Whitehead Institute/MIT Center for Genome
Research 320 Charles Street, Cambridge, MA 02141, USA
On Sep 3, 2002 this sequence version replaced gi:122474954.

All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WTB8
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L24596
Center clone name: 3038_L12

Only the first 91.9 kb of this clone are being submitted.
The remainder overlaps accession number AC055860 (WIGR project
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 Unpublished

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 Direct Submission
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 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
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 Direct Submission

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Submitted (05-SEP-2002) Whitehead Institute/MIT Center for Genome
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On Oct 1, 2002 this sequence version replaced gi:22726159.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L12764
Center clone name: L13_D_6

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ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 192618)
 TITLE Waterston, R.H.
 AUTHORS The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 192618)
 TITLE Waterston, R.H.
 AUTHORS Direct Submission
 JOURNAL Submitted (04-JUN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Jul 19, 2000 this sequence version replaced gi:9211362.

COMMENT ----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Project Information -----
 Center project name: H NH0206C01
 Summary Statistics -----
 Sequencing vector: M13; 93%
 Chemistry: Dye-primer ET; 93% of reads
 Chemistry: Dye-terminator Big Dye; 7% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 179082 bases at least Q40
 Consensus quality: 183120 bases at least Q30
 Consensus quality: 185448 bases at least Q20
 Insert size: 205000; agarose-fp
 Insert size: 190318; sum-of-contrigs
 Quality coverage: 3.99 in Q20 bases; agarose-fp
 Quality coverage: 4.34 in Q20 bases; sum-of-contrigs

* NOT: This is a 'working draft' sequence. It currently
 * consists of 24 contrigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contrigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 * 17877 17976: gap of unknown length
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 * 21535 21634: gap of unknown length
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 VERSION
 KEYWORDS HTG.

SOURCE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 Homo sapiens chromosome 11, clone RP11-583P24
 Unpublished
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 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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 Submitted (08-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
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 Direct Submission
 Submitted (19-APR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
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 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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REFERENCE	1 (bases 1 to 165490)
AUTHORS	DOE Joint Genome Institute.
TITLE	Sequencing of Human Chromosome 5
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 165490)
AUTHORS	DOE Joint Genome Institute.
TITLE	Direct Submissions
JOURNAL	Submitted (04-FEB-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT	-----Genome Center

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Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 1518520
Center clone name: RPCI-11_583F22
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Summary Statistics
 Consensus quality: 147035 bases at least Q40
 Consensus quality: 155210 bases at least Q30
 Consensus quality: 158567 bases at least Q20
 Estimated insert size: 1757000; agarose-fp estimation
 Estimated insert size: 164390; sum-of-contigs estimation
 Quality coverage: 3.94 in Q20 bases; agarose-fp estimation
 Quality coverage: 4.19 in Q20 bases; sum-of-contigs estimation
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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*	1250	1349:	gap of unknown length	
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*	3681	3780:	gap of unknown length	
*	3781	6686:	contig of 2888 bp in length	
*	6686			
*	6769	10786:	gap of unknown length	
*	6769	10866:	contig of 4098 bp in length	
*	10867	10966:	gap of unknown length	
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*	17020	17119:	gap of unknown length	
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ACCESSION COB15414
VERSION COB15414.1 GI:48144069
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REFERENCE 1
AUTHORS Golz, S., Brueggemeier, U., Geerts, A. and Thiele, R.
TITLE Diagnostics and Therapeutics for diseases associated with human
JOURNAL mas-related gene x1 (mrx1)
Patent: WO 2004042402-A 1 21-MAY-2004;
Bayer Healthcare AG (DB)
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LOCUS AX299143
DEFINITION Sequence 15 from Patent WO0183555.
ACCESSION AX299143
VERSION AX299143.1 GI:17129051
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 Anderson, D.J., Dong, X., Zylka, M., Han, S.K. and Simon, M.
Pain signaling molecules
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JOURNAL CALIFORNIA INSTITUTE OF TECHNOLOGY (US)
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Best Local Similarity 91.4%; Pred. No. 0;
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 DONG, X., HAN, S., ZYLKA, M.J., SIMON, M.I. and ANDERSON, D.J.
 A diverse family of GPCRs expressed in specific subsets of
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 Cell 106 (5), 619-632 (2001)
 JOURNAL MEDLINE 21435808
 PUBMED 11551509
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 DONG, X., HAN, S.-K., ZYLKA, M.J., SIMON, M.I. and ANDERSON, D.J.
 Direct Submission
 Submitted (19-JUN-2001) Division of Biology, 216-76, California
 Institute of Technology, 1201 E. California Blvd., Pasadena, CA
 91125, USA
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 Query Match 56.7%; Score 1483.8; DB 9; Length 2040;
 Best Local Similarity 91.4%; Pred. No. 0;
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QY	Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS
QY	1662	TCCTCGATATTTACCAATACATTTTCCCTGTATCTGCATGAATCTTCTACTGAA	1662 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1498	TCCTCGATATTTACCAACACATTTTCCCTGTATCTGCATGAATCTTCTACTGAA	1498 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
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QY	1558	CACCTTTTCTGCATATTTCTTTGTATATTAAGAGAGTCTGTGCACACCTTAAACCT	1558 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1782	TCCTTATATCTGTCTTCTACTGATAGTATCAAAAAGAGAGTCTTATTAATCTGCA	1782 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1617	TCCTTATATCTGTCTTCTACTGATAGTATCAAAAAGAGAGTCTTATTAATCTGCA	1617 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1642	GACATATGTTCCCTGAAATATCATGTTCCCTTTATATGATGAGGATATACGAGTTGGA	1642 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1677	GACATATGTTCCCTGAAATATCATGTTCCCTTTATATGATGAGGATATACGAGTTGGA	1677 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1902	AGCTCAATCTTAAATATGATGATGTTCTGTACTCTTAAATTCATGATGATGATGATG	1902 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1737	AGCTCAATCTTAAATATGATGATGTTCTGTACTCTTAAATTCATGATGATGATGATG	1737 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
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QY	2022	TTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2022 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
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QY	2082	TCCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2082 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
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QY	2202	ATTGGA 2208	2202 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	2034	ATTGGA 2040	2034 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1662	TCCTCGATATTTACCAATACATTTTCCCTGTATCTGCATGAATCTTCTACTGAA	1662 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1498	TCCTCGATATTTACCAACACATTTTCCCTGTATCTGCATGAATCTTCTACTGAA	1498 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
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QY	1617	TCCTTATATCTGTCTTCTACTGATAGTATCAAAAAGAGAGTCTTATTAATCTGCA	1617 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1642	GACATATGTTCCCTGAAATATCATGTTCCCTTTATATGATGAGGATATACGAGTTGGA	1642 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1677	GACATATGTTCCCTGAAATATCATGTTCCCTTTATATGATGAGGATATACGAGTTGGA	1677 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1902	AGCTCAATCTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1902 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1737	AGCTCAATCTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1737 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1962	AAGCAAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1962 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		
QY	1797	GAGCAAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1797 bp	1697 bp	mRNA	linear	PRI 30-JUN-2004		

QY	DB	517
457	327	
<p>Query Match 49.7%; Score 1300.2; DB 9; Length 1697; Best Local Similarity 99.0%; Pred. No. 3.9e-309; Matches 1308; Conservative 0; Mismatches 13; Indels 0; Gaps 0;</p>		
<p>ORIGIN</p>		
<p>gene</p>		
<p>CDs</p>		
<p>FEATURES</p>		
<p>source</p>		
<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.lnl.gov Series: IRAK Plate: 141 Row: m Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16876452. Location/Qualifiers 1. 1697 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:75450 IMAGE:30383708" /issue_type="Testis" /clone_lib="NIH MGC_180" /lab_host="DH10B" /note="Vector: pCMV-SPORT6.1" 1. 1697 /gene="MRGX3" /db_xref="LocustID:117195" /db_xref="MIM:607229" 362. 1330 /gene="MRGX3" /codon_start=1 /product="G protein-coupled receptor MRGX3" /protein_id="AAH67292.1" /db_xref="GI:45501077" /db_xref="LocustID:117195" /db_xref="MIM:607229" /translation="MDSTIPVLGTETLPINGRRETPCYKOTLSFTGLCTIVSLVALTGS NAVALILGGRMRNNAISYILNVLVADPLFLSGHILRSPLRLINIHPSKILSPVMVMS TFEPFGLISMLAISITRRCISLIPVIHYORRPRVLSWVCIVLMLSLRSLTEWME CDPLFGASDVWCETSDPFTITAMIVPLVCSSIVLIVRLICGSKMPLTLYITII LTVLVPLCGLPFGIOWALFSRIHMDKVLFCVHLVLSIFLSLNSANPIITFFVGL SFRORORNIKLVLORALODTPEVDEGGQLPQETLLESGSRLEQ"</p>		
<p>REMARK</p>		
<p>COMMENT</p>		
<p>JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL</p>		
<p>Generation and initial analyses of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 1247932 2 (bases 1 to 1697) Strauberg, R. Direct Submission Submitted (12-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: Dr. Michael Brownstein cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Telka Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Pribu, Parvaneh Saedi, JR Santos, Angélique Scherch, Ursula Skalske, Duane Smalau, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.</p>		

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Db      627  ATATCGCGCATCCCATCTCAAAATCTCAGTCCTGAGTCAGACCTTCCCTTATATAG 686
Qy      817  GCTTACAGCAGTCGAGCGCCATCAGACCGAGCGCTGCTTCATCTGTGGCCCATCT 876
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Qy      877  GGTACCACTGCGCGCGCCCAATACCTGTCAATCGATCATGTGTCTGCTGTGGGCC 936
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ACCESSION
VERSION
KEYWORDS
SOURCE
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Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 189230)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-1081L13
Unpublished
2 (bases 1 to 189230)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
McCarthy, M., Minova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Brown, A., Camarata, J., Campiano, A., Chang, J., Chazaro, B.,
Chapel, Y., Colangelo, M., Collins, J., Collymore, A., Cook, A.,
Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Hulse, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kelle, C., Laroque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,
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Menus, L., Minova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Riese, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Teelaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainou, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submision
Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 189230)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Bouhgalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,
Chazaro, B., Chapel, Y., Colangelo, M., Collins, J., Collymore, A.,
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Raymond, C., Retta, R., Rieback, M., Riley, R., Riese, C., Rogov, P.,

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TITLE	ROMAN, J., ROSETELI, M., ROY, A., SANTOS, R., SCHAUER, S., SCHUPBACK, R., SEAMAN, S., SEVERY, P., SPENCER, B., STANGE, R., STRAUSMAN, N., STOJANOVIC, N., STRAUSS, N., SUBRAMANIAN, A., TALAMAS, J., TESTAYE, S., THEODORE, J., TOPHAM, K., TRIVERS, M., TRAVIS, J., TRIGILLO, J., VASILIEV, H., VIEL, R., VO, A., WILSON, B., WU, X., WYMAN, D., YE, W. J., YOUNG, G., ZAINOUN, J., ZEMBECK, L., ZIMMER, A. and ZODY, M.
JOURNAL	Direct Submission
REFERENCE	Submitted (26-APR-2002). Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS	4 (bases 1 to 189230)
TITLE	Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL	On May 13, 2002 this sequence version replaced gi:20330974.
COMMENT	All repeats were identified using RepeatMasker: Smt, A.F.P.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
TITLE	Genome Center
JOURNAL	Center: Whitehead Institute/ MIT Center for Genome Research
COMMENT	Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: L21856 Center clone name: 1081_L_13 -----
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Best Local Similarity 78.7%; Pred. No. 5,1e-291;
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Db 17655 TCTCATATGCTGCTCTCATCTGATGACCTGTGACAGCTGAGAGAAATGAGTCATTT 17714
QY 635 GCTGCGCTCGCGGGCTGCGGATGAGAGAGAGCTGCTCATCTACATCTCAACCT 694
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REFERENCE
AUTHORS
TITLE
JOURNAL
Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A 1273 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JIP) / Center for Advanced Science and Technology Incubation, Ltd.
(JIP)
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REFERENCE
AUTHORS
TITLE
JOURNAL
Zhao, Q., Beasley, E.M. and Wei, M.H.
Isolated human g-protein coupled receptors, nucleic acid molecules
encoding human gpcr proteins, and uses thereof
Patent: WO 0234914-A 3 02-MAY-2002;
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Search completed: October 29, 2004, 13:55:27
 Job time : 10834 secs


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DE      Human MrgX1 (mas-related gene) DNA.
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KW      Human; mas-related gene; G-protein coupled receptor; drg-12 protein;
receptor; sensory perception; pain; analgesic; MrgX1; gene; ds.
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OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
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XX      PI      Anderson DJ, Dong X, Zylka M, Han S, Simon M;
XX      DR      WPI, 2002-171346/22.
XX      DR      P-PSDB; AAE21288.
XX
XX      PT      Isolated polypeptide, Mrg, which is a G-protein coupled receptor and an
XX      PT      isolated polypeptide, drg-12, which is also a receptor, useful for
XX      PT      identifying agonists or antagonists for treating pain.
XX

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PS Disclosure; Page 113-115; 185bp; English.

XX The invention relates to Mg (magnesium-related gene) protein, which is a G-protein coupled receptor and drug-12 protein, which is a receptor. The invention is useful for identifying compounds that bind to it, especially agonists or antagonists. Administration of an agent (e.g., the identified agonist) that increases the expression of Mg in a mammal may be used for treating impaired sensory perception in a mammal, especially pain. The antagonist may also be useful for treating impaired sensory perception in a mammal. The present sequence is human MrgX1 DNA

XX Sequence 2040 BP; 455 A; 517 C; 457 G; 611 T; 0 U; 0 Other;

Query Match 56.7%; Score 1483.8; DB 6; Length 2040;

Best Local Similarity 91.4%; Pred. No. 0;

Matches 1596; Conservative 0; Mismatches 147; Indels 4; Gaps 2;

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Qy 522 GAATGACACCAATCAACGAGACGAGGAGTCTCTTCTCAACAGCAGACCTTGAAGTTC 581
Dy 358 GAATGACACCAATCAACGAGACGAGGAGTCTCTTCTCAACAGCAGACCTTGAAGTTC 417
Qy 582 ACGGGGCTGAGTGGATGTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 641
Dy 418 ACGGGGCTGAGTGGATGTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 477
Qy 642 CTCCTGGGCTGCGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 701
Dy 478 CTCCTGGGCTGCGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 537
Qy 702 GCCGATCT 761
Dy 538 GCAAGCT 597
Qy 762 CGGATCCATCT 821
Dy 598 CGGATCCATCT 657
Qy 822 AGCATGCTGAGGCGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 881
Dy 658 AGCATGCTGAGGCGGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 717
Qy 882 CACTGCG 941
Dy 718 CGCTGCG 777
Qy 942 CTGCTGCGGAGTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1001
Dy 778 CTGCTGCGGAGTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 837
Qy 1002 GTTGTGTGTGAAGTCAAGTCT 1061
Dy 838 GTTGTGTGTGAAGTCAAGTCT 897
Qy 1062 GTTGTGTGTGAAGTCAAGTCT 1121
Dy 898 GTTGTGTGTGAAGTCAAGTCT 957
Qy 1122 GTGACAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1181
Dy 958 GTGACAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1017
Qy 1182 CCCCTTGGCATTCAGTGGGCTGT 1241
Dy 1018 CCCCTTGGCATTCAGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1077
Qy 1242 TGTGATGTGATCTAGT 1301
Dy 1078 TGTGATGTGATCTAGT 1137

Qy 1302 ATTACTCTCTCTGAGGCTCTCTTAGGACGCTCAAAATAGGAGAACTGAGCTGGTT 1361
Dy 1138 ATTACTCTCTCTGAGGCTCTCTTAGGACGCTCAAAATAGGAGAACTGAGCTGGTT 1197
Qy 1362 CTCAGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1421
Dy 1198 CTCAGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1257
Qy 1422 GAAACCTGAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1481
Dy 1258 GAAATCTGAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1317
Qy 1482 GACAGACTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1541
Dy 1318 GACAGACTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377
Qy 1542 GCTTGTGCTCAGAAATGTCTCAGTGTCTCTCAGTGTCTCTCAGTGTCTCTCAGTGTCT 1601
Dy 1378 GCTTGTGCTCAGAAATGTCTCAGTGTCTCTCAGTGTCTCTCAGTGTCTCTCAGTGTCT 1437
Qy 1602 ACCGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1661
Dy 1438 ACCGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1497
Qy 1662 TCTCTGATATTAACCAATATTTCTCTGATATTTCTGACAGTATCTTCTCTCTCTCT 1721
Dy 1498 TCTCTGATATTAACCAATATTTCTCTGATATTTCTGACAGTATCTTCTCTCTCTCTCT 1557
Qy 1722 CACTTTTCTGACCTTTTCAATTTGATTAATAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1781
Dy 1558 CACTTTTCTGACCTTTTCAATTTGATTAATAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1616
Qy 1782 TCTTTATATCTGTTTCT 1841
Dy 1617 TCTTTATATCTGTTTCT 1676
Qy 1842 GACTATGTTCCCTGAAATCATGTTCCCTTTATGATGAGGAGGAGGAGGAGGAGGAGGAG 1901
Dy 1677 GACTATGTTCCCTGAAATCATGTTCCCTTTATGATGAGGAGGAGGAGGAGGAGGAGGAG 1736
Qy 1902 AGCTCAATCTTAATAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1961
Dy 1737 AGCTCAATCTTAATAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1796
Qy 1962 AAGCAAAATATATGACCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2021
Dy 1797 AAGCAAAATATATGACCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1856
Qy 2022 TTTTATGATAGGCT 2081
Dy 1857 TTTTATGATAGGCT 1916
Qy 2082 TCTATGAAAGCAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2141
Dy 1917 TCTATGAAAGCAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1976
Qy 2142 TCTGAGTATGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2201
Dy 1977 TCTGAGTATGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2033
Qy 2202 ATTGAAA 2208
Dy 2034 ATTGAAA 2040

RESULT 4
ADH08519
ID ADH08519 standard; DNA; 2040 BP.
XX ADH08519;
AC ADH08519;
XX ADH08519;
DT 25-MAR-2004 (first entry)
XX

DE DNA sequence Mrx1.
XX mas-related gene D; Mrpd; Analgesic; Vulnerary; Ophthalmological;
KW sensory perception; glaucoma; Mrg; ds.
XX Mub musculus.
OS WO2004003133-A1.
PN 08-JAN-2004.
PD 13-MAY-2003; 2003WO-US015004.
PF 26-JUN-2002; 2002US-00183116.
PR (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX PA
XX PI Anderson DJ, Dong X, Zylka M, Han S, Simon MI;
XX WPI; 2004-083025/08.
XX DR P-PSDB; ADH08520.
XX
XX New mas-related gene D polypeptides, useful as therapeutics or in
PT identifying agonists or antagonists that alter pain perception in a
PT mammal for treating impaired sensory perception, e.g. chronic intractable
PT pain or neuropathic pain.
PS Disclosure; SEQ ID NO 15; 220pp; English.
XX
XX The present invention relates to an isolated mas-related gene D (Mrpd)
CC polypeptide. The Mrpd polypeptides are useful as therapeutics or for
CC identifying compounds, i.e. agonists or antagonists, that alter pain
CC perception in a mammal. The compounds are useful for treating impaired
CC sensory perception, e.g. chronic intractable pain or neuropathic pain,
CC promoting wound healing, restoring normal sensitivity following injury,
CC or treating ocular conditions, particularly those associated with
CC pressure such as glaucoma. The Mrp genes or proteins may be used as
CC molecular probes for the detection of cells or tissues related to or
CC involved with sensory perception. The present sequence represents a MrpA
CC (Mrg subfamily) encoding sequence.
XX
SQ Sequence 2040 BP; 455 A; 517 C; 457 G; 611 T; 0 U; 0 Other;
Query Match 56.7%; Score 1483.8; DB 12; Length 2040;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 1596; Conservative 0; Mismatches 147; Indels 4; Gaps 2;
QY 462 TCATGGGTGATGAGCTGGGGTTTCTGAGATGATTCACCATCCAGCTTGGGTACA 521
DB TCCAGGGTCCACCACTAGGGTTTCTGAGATGATTCACCATCCAGCTTGGGTACA 357
QY 522 GAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 581
DB GAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 417
QY 582 ACGGGGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 641
DB ACGGGGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
QY 642 CTCCTGGGCTGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 701
DB CTCCTGGGCTGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 537
QY 702 GCCGACCTGCTCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 761
DB GCCGACCTGCTCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 557
QY 762 CGCCATCCCATCTCCAAAATCTCTAGTCTGTGATGACCTTTCTCTAATTATAGGCTTA 821
DB CGCCATCCCATCTCCAAAATCTCTAGTCTGTGATGACCTTTCTCTAATTATAGGCTTA 598
QY 822 AGCATGCTGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 881

DB 658 AGCTTTCTGAGTCCGCTGACGACGACGACGACGACGACGACGACGACGACGACGAC 717
QY 882 CACTGCG 941
DB CGCTGCG 718
QY 942 CTGCTGCG 1001
DB CTGCTGCG 778
QY 1002 GTTTGGTGGAAAGCGACGATTTCAATTAATCCGCGCGCGCGCGCGCGCGCGCGCGCG 1061
DB GTTTGGTGGAAAGCGACGATTTCAATTAATCCGCGCGCGCGCGCGCGCGCGCGCGCG 838
QY 1062 CTCTGCG 1121
DB CTCTGCG 898
QY 1122 CTGACGAGGCTGTAGTGACATCTCTCAGAGTGTCTCTCTCTCTCTCTCTCTCTCT 1181
DB CTGACGAGGCTGTAGTGACATCTCTCAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCT 958
QY 1182 CCCTTTGGGATTCAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1241
DB CCCTTTGGGATTCAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1018
QY 1242 TGTATGTCATCTAGTTTCATTTTCATTTTCATTTTCATTTTCATTTTCATTTTCATTT 1301
DB TGTATGTCATCTAGTTTCATTTTCATTTTCATTTTCATTTTCATTTTCATTTTCATTT 1078
QY 1302 ATTTACTTTCTGTGGGCTCTTTTGGGAGGCTCAAAATAGGAGAACTTGAAGTGTGT 1361
DB ATTTACTTTCTGTGGGCTCTTTTGGGAGGCTCAAAATAGGAGAACTTGAAGTGTGT 1138
QY 1362 CTCGAGGAGCTCTGAGGACGACGCGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1421
DB CTCGAGGAGCTCTGAGGACGACGCGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1198
QY 1422 GAAACCTTGAGAGCTGTGCGGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAG 1481
DB GAAACCTTGAGAGCTGTGCGGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258
QY 1482 GACAGAGCTTTGAGAGCAATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1541
DB GACAGAGCTTTGAGAGCAATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1318
QY 1542 GCGTCTGCTGAGAAATGCTCAGTGGTCCCTCAAGGCTTCAATGATGATTTATCTA 1601
DB GCGTCTGCTGAGAAATGCTCAGTGGTCCCTCAAGGCTTCAATGATGATTTATCTA 1378
QY 1602 ACCGACAGTTGACGATTTTCAACCAATGGAAGCATTAATCTGACAGTAAATGTTGGAT 1661
DB ACCGACAGTTGACGATTTTCAACCAATGGAAGCATTAATCTGACAGTAAATGTTGGAT 1438
QY 1662 TCTCTTGAATTAACAATATCTTCTGTATCTTGTGACGAAATCTTTCTCTAATGAA 1721
DB TCTCTTGAATTAACAATATCTTCTGTATCTTGTGACGAAATCTTTCTCTAATGAA 1498
QY 1722 CACTTTTCTGACATTTTCAATGTAATAAAGAGTGTGCAACACCTTAAACTCT 1781
DB CACTTTTCTGACATTTTCAATGTAATAAAGAGTGTGCAACACCTTAAACTCT 1558
QY 1782 TCTTTATCTGTTTCTTCACTGATATATCAAAAAGAGATTTCTTATTAATCTGTCA 1841
DB TCTTTATCTGTTTCTTCACTGATATATCAAAAAGAGATTTCTTATTAATCTGTCA 1617
QY 1842 GACTATGTTCCCTGAAATCATGTTCCCTTTTATGACTGAGAGCATTAATCTGAGTTGA 1901
DB GACTATGTTCCCTGAAATCATGTTCCCTTTTATGACTGAGAGCATTAATCTGAGTTGA 1677
QY 1902 AGCTAAATCTTAATAGAGATGCTGACTCACTTAATCTGATTAATCTGATTAATCTGAT 1961
DB AGCTAAATCTTAATAGAGATGCTGACTCACTTAATCTGATTAATCTGATTAATCTGAT 1737


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QY 942 CTGCTGCGAGATATCTGAGAGTGAATGTTCTGTGAATCTCTGTTTAAAGTGTGCTGATCT 1001
DB 778 CTGCTGCGAGATATCTGAGAGTGAATGTTCTGTGAATCTCTGTTTAAAGTGTGCTGATCT 837
QY 1002 GTTGTGTGAAGATGATGATTTCAATCAATGAGTGTGCTGTTTAAAGTGTGCTGATCT 1061
DB 838 GCTTGTGTGAAGATGATGATTTCAATCAATGAGTGTGCTGTTTAAAGTGTGCTGATCT 897
QY 1062 CTGTGTGAGTCAAGCTGTGTCTGTGTGAGATTTCTGTGTGATCTCCGGAAGATGCTG 1121
DB 898 CTGTGTGAGTCAAGCTGTGTCTGTGTGAGATTTCTGTGTGATCTCCGGAAGATGCTG 957
QY 1122 CTGACAGAGCTGTGTGATGATGATCTCTCTCAAGTGTGTGCTCTCTCTGTGTGCTG 1181
DB 958 CTGACAGAGCTGTGTGATGATGATCTCTCTCAAGTGTGTGCTCTCTCTGTGTGCTG 1017
QY 1182 CCTTGTGAGATGATGATGAGGCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1241
DB 1018 CCTTGTGAGATGATGATGAGGCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1077
QY 1242 TGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1301
DB 1078 TGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137
QY 1302 ATTTACTTCTGTGTGAGTCTCTGTGTGAGAGCTGATGATGATGATGATGATGATGATGAT 1361
DB 1138 ATTTACTTCTGTGTGAGTCTCTGTGTGAGAGCTGATGATGATGATGATGATGATGATGAT 1197
QY 1362 CTCAGAGAGGCTGTGTGAGAGAGCTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGT 1421
DB 1198 CTCAGAGAGGCTGTGTGAGAGAGCTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGT 1257
QY 1422 GAAACCTGTGAGAGCTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1481
DB 1258 GAAACCTGTGAGAGCTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1317
QY 1482 GACGAGATCTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGT 1541
DB 1318 GACGAGATCTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGT 1377
QY 1542 GCTTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGT 1601
DB 1378 GCTTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGT 1437
QY 1602 ACCTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1661
DB 1438 ACCTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
QY 1662 TCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1721
DB 1498 TCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
QY 1722 CACTTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1781
DB 1558 CACTTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1616
QY 1782 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1841
DB 1617 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1676
QY 1842 GACTATGTTCCCTGAGAAATCATGTTCCCTTTTATGATGATGATGATGATGATGATGAT 1901
DB 1677 GACTATGTTCCCTGAGAAATCATGTTCCCTTTTATGATGATGATGATGATGATGATGAT 1736
QY 1902 AGCTCAATTTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1961
DB 1737 AGCTCAATTTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1796
QY 1962 AAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2021
DB 1797 GAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1856
QY 2022 TTTTATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2081

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DB 1857 TTTTATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1916
QY 2082 TCTAATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2141
DB 1917 TCTAATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1976
QY 2142 TCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2201
DB 1977 TCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2033
QY 2202 ATTTGAA 2208
DB 2034 ATTTGAA 2040

RESULT 6
ADC86820
ID ADC86820 standard; DNA; 1369 BP.
XX
XX ADC86820;
AC
XX
XX 01-JAN-2004 (first entry)
DT
XX
DE Human GPCR gene SEQ ID NO:1273.
XX
XX de; gene; human; GPCR;
XX KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX BPI270724-A2.
PN
XX
XX 02-JAN-2003.
PD
XX
XX 18-JUN-2002; 2002EP-00013517.
PF
XX
XX 18-JUN-2001; 2001JP-00246789.
PR
XX
XX (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NAD-) NAT INST ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX Suwa M, Arai K, Akiyama Y, Aburatani H;
PI
XX
XX WPI; 2003-315783/31.
DR P-PSDB; ADC86821.
XX
XX
XX New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 1273; 28bp; English.
PS
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.
XX
XX
XX Sequence 1369 BP; 272 A; 372 C; 340 G; 385 T; 0 U; 0 Other;
SQ
XX
XX
XX Query Match 45.6%; Score 1192.6; DB 10; Length 1369;
XX Best Local Similarity 99.7%; Pred. No. 0;
XX Matches 1195; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 462 TCATGGGTCATGAGCTGGGGTTCGTGAGCATGATTCACCATCCAGTCTTGGGTACA 521
DB 171 TCAGGGTCATGAGCTGGGGTTCGTGAGCATGATTCACCATCCAGTCTTGGGTACA 230
QY 522 GAATGACCAATCAACGAGCTGAGAGATCTCTTGTACAGACGACCTGAGCTTC 581

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Db 231 GAACTGACACCAATCAACGACGAGAGAGCTCTCTGCTCAAGACAGACCTGAGCTTC 290
QY 582 ACCGGGGCTGACGATGATGCTTCCCTGTGCGGCTGACAGAAACGCGGTGCTCTGCG 641
Db 291 ACCGGGGCTGACGATGATGCTTCCCTGTGCGGCTGACAGAAACGCGGTGCTCTGCG 350
QY 642 CTCCTGGGGCTGCGCAGATGCGAGAAACGCTGTCTCAATCTCAATCTTCAACCTGATCGCG 701
Db 351 CTCCTGGGGCTGCGCAGATGCGAGAAACGCTGTCTCAATCTCAATCTTCAACCTGATCGCG 410
QY 702 GCCGACTTCTCTTCTTAAAGCGCCACATTATATGTTGCGCGTTACCGCTCATCAATATC 761
Db 411 GCGCACTTCTCTTCTTAAAGCGCCACATTATATGTTGCGCGTTACCGCTCATCAATATC 470
QY 762 CGCCATCCCAATCTCAAAATCTCAATCTGATGATGATGATGATGATGATGATGATGATGAT 821
Db 471 CGCCATCCCAATCTCAAAATCTCAATCTGATGATGATGATGATGATGATGATGATGATGAT 530
QY 822 AGCATGCTGACGCGCATGACGACGAGCGCTGCTGCTCATCTGATGCGCCATCTGATC 881
Db 531 AGCATGCTGACGCGCATGACGACGAGCGCTGCTGCTCATCTGATGCGCCATCTGATC 590
QY 882 CACTGCGCGCGCCCAAGATACCTGTCAATGATGATGATGATGATGATGATGATGATGATGAT 941
Db 591 CACTGCGCGCGCCCAAGATACCTGTCAATGATGATGATGATGATGATGATGATGATGATGAT 650
QY 942 CTGCTGCGGAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1001
Db 651 CTGCTGCGGAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 710
QY 1002 GTTGTGATGAAAGCTGAGATTTTCAATATGCGGAGCTGATTTTATATGATGATGAT 1061
Db 711 GTTGTGATGAAAGCTGAGATTTTCAATATGCGGAGCTGATTTTATATGATGATGAT 770
QY 1062 CTCTGAGGATCCAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
Db 771 CTCTGAGGATCCAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
QY 1122 CTGACCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1181
Db 831 CTGACCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 890
QY 1182 CCCCTTGGCATTCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1241
Db 891 CCCCTTGGCATTCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 950
QY 1242 TGTGATGATGATTCATGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1301
Db 951 TGTGATGATGATTCATGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010
QY 1302 ATTATCTTCTTCTGCGGCTCTCTTAAAGCAGGCTCAAAATAGGCGAAGCTTGAAGCTGTT 1361
Db 1011 ATTATCTTCTTCTGCGGCTCTCTTAAAGCAGGCTCAAAATAGGCGAAGCTTGAAGCTGTT 1070
QY 1362 CTCGAGAGGGCTGCGAGGACGACGCTGAGGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1421
Db 1071 CTCGAGAGGGCTGCGAGGACGACGCTGAGGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1130
QY 1422 GAAACCTGAGAGCTGCGGAGAGGATGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1481
Db 1131 GAAACCTGAGAGCTGCGGAGAGGATGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1190
QY 1482 GACAGAGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
Db 1191 GACAGAGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1250
QY 1542 GCGCTTGGCGCTCAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1601
Db 1251 GCGCTTGGCGCTCAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1310
QY 1602 ACCTGACAGTTGCAAGTTTCAACCATGAGAAAGATATGCTGACAGTACAAATGTTTGA 1660

Db 1311 ACCTGACAGTTGCAAGTTTCAACCATGAGAAAGATATGCTGACAGTACAAATGTTTGA 1369
RESULT 7
ABK52823
ID ABK52823 standard; DNA; 8622 BP.
XX
XX ABK52823;
XX
XX 27-AUG-2002 (first entry)
XX
XX Genomic DNA encoding human G-protein coupled receptor (GPCR).
DE
XX Human; G-protein coupled; receptor; GPCR; human protease;
KW human therapeutic protein; query sequence; search; gene; ds;
KW sequence database; non-human transgenic animal; gene therapy;
XX chromosome 3.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 4300..8496
FT /*tag= a
FT /product= "Human G-protein coupled receptor (GPCR)"
FT exon 4300..4319
FT /*tag= b
FT /number= 1
FT intron 4320..7502
FT /*tag= c
FT /number= 1
FT exon 7503..8496
FT /*tag= d
FT /number= 2
XX
XX W0200234914-A1.
PN
XX
XX 02-MAY-2002.
PD
XX
XX 10-OCT-2001; 2001WO-US031592.
PE
XX
XX 25-OCT-2000; 2000US-00695045.
PR
XX 31-MAY-2001; 2001US-00867570.
PR
XX
XX (PEKS) PE CORP NY.
PA
XX
XX Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM;
PI
XX WPI; 2002-463360/49.
DR
XX P-PSDB; AAU97598.
DR
XX
XX Novel isolated G-protein coupled receptor peptide useful for treating
PT disorder characterized by absence of, in appropriate or unwanted
PT expression of the receptor protein, and as immunogens to raise
PT antibodies.
XX
XX Claim 4; Fig 3; 75pp; English.
PS
XX
XX The present invention relates to a new G-protein coupled receptor (GPCR)
CC peptide. The invention is useful for identifying a modulator of GPCR and
CC for treating a disease or condition mediated by a human protease. The
CC invention is also useful as models for the development of human
CC therapeutics, for identifying therapeutic proteins, as targets for
CC development of human therapeutic agents, and as query sequence to perform
CC a search against sequence databases to, for e.g., identify other family
CC members of related sequences. The vector of the invention is useful for
CC producing a GPCR protein or peptide, for conducting cell-based assays
CC involving the GPCR protein or its fragment, for identifying GPCR protein
CC mutants whose functions are affected, and to produce non-human transgenic
CC animals. The present nucleic acid sequence represents the human G-protein
CC coupled receptor (GPCR) gene located on chromosome 3. This sequence
CC encodes the human G-protein coupled receptor (GPCR) protein of the
XX invention

QY 522 GAACGACACCAATCAACGAGAGAGAGACTCCCTGCTCAAGACAGACCCCTGAGCTTC 581
 DB 362 GAACGACACCAATCAACGAGAGAGAGACTCCCTGCTCAAGACAGACCCCTGAGCTTC 421
 QY 582 AGCGGGGCTGAGCTGAGCTGTTCCCTTGTGGGCTGACAGAGAAAGCGGCTGTGCTCG 641
 DB 422 AGCGGGGCTGAGCTGAGCTGTTCCCTTGTGGGCTGACAGAGAAAGCGGCTGTGCTCG 481
 QY 642 CTCCTGGGGCTGCGGAGTGGGAGAGAGAGCTGCTCAATCTCAATCTCAATCTGAGCTG 701
 DB 482 CTCCTGGGGCTGCGGAGTGGGAGAGAGAGCTGCTCAATCTCAATCTCAATCTGAGCTG 541
 QY 702 GCGGACTTCTCTCTCTAGGCGGACATATATATGTCGCGGTATACGCTCATCAATATC 761
 DB 542 GCGGACTTCTCTCTCTAGGCGGACATATATATGTCGCGGTATACGCTCATCAATATC 601
 QY 762 GCGGACTTCTCTCTCTAGGCGGACATATATGTCGCGGTATACGCTCATCAATATC 821
 DB 602 GCGGACTTCTCTCTCTAGGCGGACATATATGTCGCGGTATACGCTCATCAATATC 661
 QY 822 AGCATGCGAGGCGGAGTGGGAGAGAGAGCTGCTCAATCTCAATCTGAGCTGAGCTAC 881
 DB 662 AGCATGCGAGGCGGAGTGGGAGAGAGAGCTGCTCAATCTGAGCTGAGCTGAGCTAC 721
 QY 882 CACTGCGCGCGCGGACATCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 941
 DB 722 CACTGCGCGCGCGGACATCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 781
 QY 942 CTGCTGCGGAGTATCTGAGAGTGTCTGTGAATCTCTGTTATGTCGTCGATTCCT 1001
 DB 782 CTGCTGCGGAGTATCTGAGAGTGTCTGTGAATCTCTGTTATGTCGTCGATTCCT 841
 QY 1002 GTTGTGTGTGAAGGTAGATTTTCAATATCAATGCGGCGGCTGTTTATATGTCGTT 1061
 DB 842 GTTGTGTGTGAAGGTAGATTTTCAATATCAATGCGGCGGCTGTTTATATGTCGTT 901
 QY 1062 CTCTGTGGGCTCAGCTGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1121
 DB 902 CTCTGTGGGCTCAGCTGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 961
 QY 1122 CTGACGAGGCTGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1181
 DB 962 CTGACGAGGCTGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1021
 QY 1182 CCCCTTGGGCTCAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1241
 DB 1022 CCCCTTGGGCTCAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1081
 QY 1242 TGTGATGTGATCTAGTTTCAATTTTCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1301
 DB 1082 TGTGATGTGATCTAGTTTCAATTTTCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1141
 QY 1302 ATTACTTCTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1361
 DB 1142 ATTACTTCTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1201
 QY 1362 CTCGAGAGGCTCTGACGAGACAGCCCTGAGTGTGATGAGTGTGAGTGTGAGTGTGAG 1421
 DB 1202 CTCGAGAGGCTCTGACGAGACAGCCCTGAGTGTGATGAGTGTGAGTGTGAGTGTGAG 1261
 QY 1422 GAAACCTGAGCTGTGAGGAGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1481
 DB 1262 GAAACCTGAGCTGTGAGGAGAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1321
 QY 1482 GACAGAGCTTGTGAGAGATGTCCTGCTGACATTTATATATATATATATATATATAT 1541
 DB 1322 GACAGAGCTTGTGAGAGATGTCCTGCTGACATTTATATATATATATATATATATAT 1381
 QY 1542 GCCTTCTGCTGAGAAATG 1560
 DB 1382 GCCTTCTGCTGAGAAATG 1400

RESULT 9
 ABZ42595
 ID ABZ42595 standard; DNA; 1400 BP.
 XX
 AC ABZ42595;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human G protein-coupled receptor Mrx3 nucleotide SEQ ID NO:673.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PE 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burner GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-046718/04.
 XX
 DR P-PSDB; ABP81750.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 PS Disclosure; Fig 1; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (1) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42595 to ABZ42609 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX

Sequence 1400 BP; 276 A; 375 C; 363 G; 386 T; 0 U; 0 Other;


```
Db 422 ACCGGGCTGACGTCATCGTTTCCCTTGTGCGCTGACAGAAACGGGTTGCTCTGG 481
Qy 642 CTCCTGGGCTGCGGATGCGGAGAAAGCTGTCTTCATCTACATCTCAACCTGTGGC 701
Db 482 CTCCTGGGCTGCGGATGCGGAGAAAGCTGTCTTCATCTACATCTCAACCTGTGGC 541
Qy 702 GCGGACTTCTCTCTTAGGCGGCACATTATATGTTGCGCGTATAGCGCTCATCAATATC 761
Db 542 GCGGACTTCTCTCTTAGGCGGCACATTATATGTTGCGCGTATAGCGCTCATCAATATC 601
Qy 762 CGGCATCCATCTCAAAATCTCATGCTGTGATGACCTTCCCTACTTATAGGCTTA 821
Db 602 CGGCATCCATCTCAAAATCTCATGCTGTGATGACCTTCCCTACTTATAGGCTTA 661
Qy 822 AGCATGCTGAGCGCATCAGACCGAGCGCTGCTTCATCTGTGCGCCATCTGGTAC 881
Db 662 AGCATGCTGAGCGCATCAGACCGAGCGCTGCTTCATCTGTGCGCCATCTGGTAC 721
Qy 882 CACTGCGCGCGCGCGAGATACCTGTCAATGCGTCAATGTCCTGCTGGCGCTGTGC 941
Db 722 CACTGCGCGCGCGCGAGATACCTGTCAATGCGTCAATGTCCTGCTGGCGCTGTGC 781
Qy 942 CTCGTCGCGAGATATCTGAGTGTGATGTCCTGCTGTTAGTGTGCTGATTC 1001
Db 782 CTCGTCGCGAGATATCTGAGTGTGATGTCCTGCTGTTAGTGTGCTGATTC 841
Qy 1002 GTTTGTTGTAAGCAATGATTTCAATCAATCGCGTGTGTTTATATGTTGTT 1061
Db 842 GTTTGTTGTAAGCAATGATTTCAATCAATCGCGTGTGTTTATATGTTGTT 901
Qy 1062 CTCGTGCGGTCACCGTGTCTGTGTCAGATTCCTGTGATCCCGGAAGATGCG 1121
Db 902 CTCGTGCGGTCACCGTGTCTGTGTCAGATTCCTGTGATCCCGGAAGATGCG 961
Qy 1122 CTGACGAGGCTGTACGTCACCATCTCTCAAGTGTGTCCTCTCTCTGTGCGCTG 1181
Db 962 CTGACGAGGCTGTACGTCACCATCTCTCAAGTGTGTCCTCTCTCTGTGCGCTG 1021
Qy 1182 CCTTTGGCATTCAGTGGGCGCTGTTCAGATTCACCTGATGGAAGTCTTATTT 1241
Db 1022 CCTTTGGCATTCAGTGGGCGCTGTTCAGATTCACCTGATGGAAGTCTTATTT 1081
Qy 1242 TGTGATGTGATCTAGTTTCCATTTCTGTGCGCTCTTAACAGAGGCAACCCATC 1301
Db 1082 TGTGATGTGATCTAGTTTCCATTTCTGTGCGCTCTTAACAGAGGCAACCCATC 1141
Qy 1302 ATTACTTCTTCTGCGCTCTTATAGGAGGCTCAAAATAGGCAAGACTGAGT 1361
Db 1142 ATTACTTCTTCTGCGCTCTTATAGGAGGCTCAAAATAGGCAAGACTGAGT 1201
Qy 1362 CTCAGAGGGCTCTGACAGACAGCCTGAGGTGATGAGGTGAGGGTGTCTCTCAG 1421
Db 1202 CTCAGAGGGCTCTGACAGACAGCCTGAGGTGATGAGGTGAGGGTGTCTCTCAG 1261
Qy 1422 GAAACCTTGAAGCTGTGGGAGAGAGATGAGAGAGAGAAACCTGTGCGCTGCA 1481
Db 1262 GAAACCTTGAAGCTGTGGGAGAGAGATGAGAGAGAGAAACCTGTGCGCTGCA 1321
Qy 1482 GACAGACTTGAAGAGCAATCTGCGCTGACACCTTGAACAATTATGCAATTTTCTTA 1541
Db 1322 GACAGACTTGAAGAGCAATCTGCGCTGACACCTTGAACAATTATGCAATTTTCTTA 1381
Qy 1542 GCGTTTGTGCTGAGAAATG 1560
Db 1382 GCGTTTGTGCTGAGAAATG 1400
```

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RESULT 11
ADCB6444
ID ADCB6444 standard; DNA; 1369 BP.
XX
AC ADCB6444;
```

```
XX 01-JAN-2004 (first entry)
DT Human GPCR gene SEQ ID NO:897.
DE de; gene; human; GPCR;
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
OS Homo sapiens.
EN EP1270724-A2.
XX
XX 02-JAN-2003.
PD 18-JUN-2002; 2002EP-00013517.
XX
XX 18-JUN-2001; 2001JP-00246789.
PR 18-JUN-2001; 2001JP-00246789.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBARIO.
XX
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
PI WPI; 2003-315783/31.
XX
XX P-PSDB; ADCB6445.
DR
XX
XX New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 897; 28bp; English.
PS
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADCB6445-ADCB6466 encode GPCR's of the
CC invention.
XX
XX Sequence 1369 BP; 276 A; 364 C; 337 G; 392 T; 0 U; 0 Other;
SQ
XX
XX Query Match 39.7%; Score 1040.6; DB 10; Length 1369;
XX Best Local Similarity 91.7%; Pred. No. 1.1e-280;
XX Matches 1100; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
```


Qy	946	TGCGAGATACCTGAGAGGAGNATGTCGAGCTTCCTGGTTAAGAGAGNCTAATTCGTTT	1005
Db	887	TGTTTAGATACCTGAGAGGAGGTTCTGAGACTTCCTGTTAAGAGAGNCTAATTCGTTT	946
Qy	1006	GGTGTGAACCTCGAATTCATTTACAAATCGAGTGGCTGTTTTTATATGTCGTCTCT	1065
Db	947	GGTGTGAACCTCGAATTCATTTACAAATCGAGTGGCTGTTTTTATATGTCGTCTCT	1006
Qy	1066	GTGGGTCCAGCCTGGTCTCTGCTGGTCAAGATTTCTCTGTGATATCCCGAAGATGCCGCTGA	1125
Db	1007	GTGTTTCCAGCCTGGTCTCTGCTGGTCAAGATTCCTGTGATATCCCGAAGATGCCGCTGA	1066
Qy	1126	CCAGGCTGTACGTAAACCAATCCCTCCACAAAGTCGTGTTTCTCTCTCTGTGAGCTGGCT	1185
Db	1067	CCAGGCTGTACGTAAACCAATCCCTCCACAAAGTCGTGTTTCTCTCTCTGTGAGCTGGCT	1126
Qy	1186	TTGGCAATTCAGTGGGCCCTGTGTTTTCCAGAGATCCACTGGATTTGGAAGATCTTAATTTGTC	1245
Db	1127	TTGGCAATTCAGTGGGCCCTTAATTTTACAGAGATGCACCTGAATTTGGAAGATCTTAATTTGTC	1186
Qy	1246	ATGTGCATCTAATGTTTCCATTTTCTGTTCGGCTCTTAACAGCAGTGCACACCCCATCATTT	1305
Db	1187	ATGTTTATCTGTGTTTGCATGTCCCGTCTCTCTTAACAGATGTCGCAACCCCATCATTT	1246
Qy	1306	ACTTCTTCGTGGGCTCCTTTAAGGACGCTCAAAATAGGACAGACCTGAAGCTGTCTCC	1365
Db	1247	ACTTCTTCGTGGGCTCCTTTAAGGACGCTCAAAATAGGACAGACCTGAAGCTGTCTCC	1306
Qy	1366	AGAGGGCTCTGACAGACACGCTGAAGTGTGATGAAAGTGTGAGGGTGTCTCTCAGGAA	1425
Db	1307	AGAGGGCTCTGACAGACACGCTGAAGTGTGATGAAAGTGTGAGGGGACGCTCTCAGGAA	1366
Qy	1426	CCCTGTGAGCTGTCCGGAAGACAGATTGTGAGCAGTGAAGAAACCTCTGCGCT----GTCA	1481
Db	1367	GCTGTGAGCTGTCCGGAAGACAGATTGTGAGGGAATGAGGGAAGGCTCTGCGCTCTGACGTCA	1426
Qy	1482	GACAGACATTGAGAGCAATGCTGCGCTCCGACACCTTGACAAATTAATGCAATTTTTCTTA	1541
Db	1427	GACGGGACTTTGAGAGCAACTGTGCTGCAACCTTGACAAATTAATGCAATTTTTCTTA	1486
Qy	1542	GCTTTCGTGCTCAGAAATGTCTCAGTGTGCTCTCAAGGATCTTGCAATATGATGTTTATCTA	1601
Db	1487	GCGTTTGCCTCAGAAATGTCTCAGTGTGATCTCAAGGATCTTCAAAATTAATGTTTATCTA	1546
Qy	1602	ACCTGACAGTTGACGTTTTCAACCATGGAAGCAATTATGTGACAGTACAAATGTTTGG	1659
Db	1547	ACCTGACAGTTGACGTTTTCAACCATGGAAGCAATTATGTGACAGTACAAATGTTTGG	1604

RESULT 13	
AB242602	
ID	AB242602 standard; DNA; 1604 BP.
XX	
XX	AB242602;
XX	
DT	04-MAR-2003 (first entry)
XX	
DE	Human MrgX4 G protein-coupled receptor nucleotide SEQ ID NO:688.
XX	
KW	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW	G protein-coupled receptor modulator; antibody; immune-related disease;
KW	growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW	immunological-related cell proliferative disease; autoimmune disease;
KW	Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy
KW	osteoporosis; cardiovascular; inflammation; Crohn's disease; diabetes;
KW	graft versus host disease; Parkinson's disease; multiple sclerosis; pain
KW	pariasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW	ulcer; gene; de.
XX	
OS	Homo sapiens.
XX	

PN	WO200261087-A2.
XX	
PD	08-AUG-2002.
XX	
PF	19-DEC-2001, 2001WO-US050107.
XX	
PR	19-DEC-2000; 2000US-0257144P.
XX	
PA	(LIFE-) LIFESPAN BIOSCIENCES INC.
XX	
PI	Burner GC, Roush CL, Brown JP;
XX	
DR	WPI; 2003-046718/04.
XX	
DR	P-PsDB; ABP81758.
XX	
PT	New isolated antigenic peptides e.g., for G protein-coupled receptors
PT	(GPCR), useful for diagnosing and designing drugs for treating conditions
PT	in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT	autoimmune diseases.
XX	
PS	Disclosure; Fig 1; 523pp; English
XX	

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular GPCR. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.

Seq	Sequence	1604 BP; 337 A; 420 C; 399 G; 448 T; 0 U; 0 Other;
Query Match	38.7%;	Score 1013.6; DB 8; Length 1604;
Best Local Similarity	91.0%;	Pred. No. 4.5e-273;
Matches 1090;	Conservative	0; Mismatch 104; Indels 4; Gaps 1.
Qy	466	GGGCTATCAGACCTGGGGTTCTGAGCATTGATTCACCATCCCGATCTGGGGTCAGAAC 525
Db	407	GGGGCACAGACTGAGATTCTTGAGCATGATTCACACCGTCCAGGTCTTGGTCTCAAAAC 466
Qy	526	TGACACCATTAACGAGAGTGAGAGACTCTTGTCTACAGCAGACCTGAGCTTACAGG 585
Db	467	TGAACCATTAACGAGAGTGAGAGACTCTTGTCTACATCAAGACCTGAGCTTACAGG 526
Qy	586	GGCTGAGGTGATCGTTCTTCCTTGTGCGCTGACAGGAAAGCGGGTTGTGCTTGGCTCC 645
Db	527	TGCTGAGGTGATCAATTCTTCCTTGTGCGACTGACAGGAAAGCGGGTGTGCTTGGCTCC 586
Qy	646	TGGGCTGCCGATGCGGAGAACGCTGTCTTCATCTACATCTCAACTGATCGGAGCCG 705
Db	587	TGGGCTACCGGATGCGGAGAACGCTGTCTTCATCTACATCTCAACTGAGCCGAGAG 646
Qy	706	ACTTCCTCTTCTTAGGGGCGACATTAATGTTGGCGTTACGGCTACATCAATATCCGCC 765
Db	647	ACTTCCTCTTCTTAGGCTCCAGATTAACGTTGGCGATTACGGCTACATTAATATCCGCC 706

[illegible]

BR		18-JUN-2001; 2001JP-00246789.
XX		(NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA		(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX		
PI	Suwa M, Asai K, Akiyama Y, Aburatani H;	
DR	WPI; 2003-315783/31.	
XX	P-PSDB; ADC06589.	
PT	New polynucleotide, useful for preparing a composition for treating a	
PT	patient in need of increased or suppressed activity or expression of the	
FT	guanosine triphosphate-binding protein coupled receptor.	
CC	Claim 1; SEQ ID NO 1041; 28pp; English.	
XX		
XX	The invention relates to a novel polynucleotide encoding a guanosine	
CC	triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of	
CC	the invention may have a use in gene therapy. The polynucleotide and	
CC	polypeptide are useful for preparing a composition for treating a patient	
CC	in need of increased or suppressed activity or expression of the	
CC	guanosine triphosphate-binding protein coupled receptor. The	
CC	polynucleotide sequences shown in AD065548-AD067616 encode GPCR's of the	
XX	invention.	
XX		
SO	Sequence 1369 BP; 279 A; 364 C; 342 G; 384 T; 0 U; 0 Other;	
	Query Match 38.7%; Score 1012.2; DB 10; Length 1369;	
	Best Local Similarity 91.0%; Pred. No. 1e-272;	
	Matches 1088; Conservative 0; Mismatches 103; Indels 4; Gaps 1;	
OY	466 GGATCATCAGACTGCGGGTTTCTGCATGTGATTCAACCATCCAGTCCTGGGTACAGAAC	525
Dd	175 GGGGACCAGACTGAGGGTTTCTGCATGTGATTCACCCGTCCAGTCTTGSTACAATAAC	234
OY	526 TGACACCAATTAACGACGTGAGAGACTCTTGTCTACAGACAACCTTAGCTTACAG	585
Dd	235 TGACACCAATTAACGACGTGAGAGACTCTTGTCTACAAACCAACCTTAGCTTACAG	294
OY	586 GGCCTGAGTGCATGGTTTCCCTTGCCGCGCTGAAGAAAAGCGGTTGCTCGGCTCC	645
Dd	295 TGTGACGTGTATCAATTCCTTTCGGAAGTGAAGAAAGCGGTTGCTCGGCTCC	354
OY	646 TGGCTGCGCGATCGAGAACGCTGTCTTCATCTAATCTTCAACTGTCGCGCG	705
Dd	355 TGGCTACCGATCGAGAACGCTGTCTTCATCTAATCTTCAACTGTCGCGCG	414
OY	706 ACTTCTCTTCTTAGCGGCCACATTAATATGTTCCCGTTACGCTCAATCAATTCGCGC	765
Dd	415 ACTTCTCTTCTTAGCGGCCACATTAATATGTTCCCGTTACGCTCAATCAATTCGCGC	474
OY	766 ATCCCATCTCCAATAATCTTAGTCTGTGATGAGACTTTCCTACTTTATAGGCTTAACA	825
Dd	475 ATTCATCTCCGAAATCTCTGTTTCTGTGAAGACCTTTCCTACTTTAAGGCTTAAGTA	534
OY	826 TGCTGAGGCGCATCAGACCGAGGCGTGCCTGCATCTGTGAGCCCATCTGTATCAACT	885
Dd	535 TGCTGAGGCGCATCAGACCGAGGCGTGCCTGCATCTGTGAGCCCATCTGTATCAACT	594
OY	886 GCCGCGCGCCAGATACCTGTGCATCGATGTGTCTGTGCTGTGCGCCCTGTCTCCGTC	945
Dd	595 GCCGCGCGCCAGATACCTGTGCATCGATGTGTCTGTGCTGTGCGCCCTGTCTCCGTC	654
OY	946 TGCAGAGTATCTGTGAGTGAATGTTCTGTGACTTCCCTGTTTAAAGTGTCGATCTGT	1005
Dd	655 TGTATTAGTATCTGTGAGTGAATGTTCTGTGACTTCCCTGTTTAAAGTGTCGATCTGT	714
OY	1006 GTGTGAAGAGTCAAGATTCTATTAACATCGAGTGGCTGTTTTTAAAGTGTCGATCT	1065
Dd	715 GTGTGAAGAGTCAAGATTCTATTAACATCGAGTGGCTGTTTTTAAAGTGTCGATCT	774
OY	1066 GTGGATCGAGCTGTCTGTGTGATGAGATTCTGTGATGCCGGAAGATGCCGCTGA	1125


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Db      775 GTGTTTCCAGCCTGCTCTCTGCTGACGATCCTCTGAGATCCCGAAGATGCCGCTGA 834
Qy      1126 CCAGGCTGTAGTGAACAATCTCTCAACAGTGTGCTCTCTCTCTGTGAGCTGCCCT 1185
Db      835 CCAGGCTGTAGTGAACAATCTCTCAACAGTGTGCTCTCTCTCTGTGAGCTGCCCT 894
Qy      1186 TTGGATTCAGTGGGCGCTGTTTCCAGAGATCCACTGGATGGAAGTCTTATTTTTC 1245
Db      895 TCGGCATTCGTGGGGCGCTTAATTTACAGATGACCTGAATTTGGAAAGTCTTATTTTC 954
Qy      1246 ATGTCATCTAGTTCCTCCATTTTCCGTGCTCTTAACAGCAGTGCACCAACCCATCATTT 1305
Db      955 ATGTTTATCTGATTTGCAATGCTCTCTCTTAACAGTATGCAACCCATCATTT 1014
Qy      1306 ACTTCTTGCTGGGCTCTCTTTAGGCAAGCTCAAAATAGGCAAACTGAAGCTGTTCTCC 1365
Db      1015 ACTTCTTGCTGGGCTCTCTTTAGGCAAGCTCAAAATAGGCAAACTGAAGCTGTTCTCC 1074
Qy      1366 AGAGGGCTCTGCAAGCAAGCCTGAGATGATGAAGTGAAGGCTGCTTCTCAGGAAA 1425
Db      1075 AGAGGGCTCTGCAAGCAAGCCTGAGATGATGAAGTGAAGGCTGCTTCTCAGGAAA 1134
Qy      1426 CCTGAGCTGTGGGGAAGCAATGAGAGCAATGAGGAAGAACTCTGCGCT---GTCA 1481
Db      1135 GCTTGAGCTGTGGGGAAGCAATGAGGAGCAATGAGGAGAGCTCTGCGCTGTCAATCA 1194
Qy      1482 GACAGACTTTGAGAGCAATGCTGCGCTGCAACCTTGAACAATATATGCAATTTTCTTA 1541
Db      1195 GACGGGACTTTGAGAGCAACTGTCTCTGCAACCTTGAACAATATATGCAATTTTCTTA 1254
Qy      1542 GCTTCTGCTGAGAAATGTCTCAAGTGTCTCTCAAGTCTTGAATGATGTTTATCTA 1601
Db      1255 GCGTTTCGCTCAGAAATGTCTCAGTGTACTCAAGTCTTCAAAATTAATGTTTATCTA 1314
Qy      1602 ACCTGACAGTGCATTTTCAACCATGAAAGCATTAATGCTGACAGTACATGTT 1656
Db      1315 ACCTGACAGTGCATTTTCAACCATGAAAGCATTAATGCTGACAGTACATGTT 1369

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Search completed: October 29, 2004, 10:54:55
 Job time : 1234 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 10:12:37 : Search time 7917 Seconds
(without alignments)
12049.920 Million cell updates/sec

Title: US-09-867-570-1

Sequence: 1 aacatctgcgcgcgaattcg.....gaaaaaaaaaaaaaaaaa 2618

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	709.2	27.1	889	6	CA455045
2	663.2	25.3	883	7	CN835944
3	606	23.1	835	7	CN843633
4	604.4	23.0	764	4	BG198766
5	603.2	23.0	827	7	CN831885
6	598.2	22.8	924	7	CN839634
7	586.8	22.4	688	2	BE439409
8	562.6	21.5	662	1	AV731610
9	548.2	20.9	787	4	BG208126
10	544.6	20.8	825	7	CN843258
11	516	19.7	871	7	CN839125
12	504.6	19.3	953	7	CN839765
13	486.4	18.6	871	4	BG210740
14	483.4	18.5	924	6	CD051096
15	468.8	17.9	1009	6	CN837763
16	453.8	17.3	552	8	AQ392205
17	377.6	14.4	895	8	CN840024
18	366	14.0	716	9	AG183584
19	362.4	13.8	811	8	AQ888076
20	358.8	13.7	503	8	AQ888076
21	347	13.3	2075	8	B74348
22	346.2	13.2	2075	8	AK029369
23	344	13.1	725	6	CD468987
24	336.8	12.9	719	6	CD469292

25	335.4	12.8	620	8	AQ696198
26	324.4	12.4	905	6	CD243595
27	318.6	12.2	644	6	CD469930
28	316.6	12.1	644	6	CD470186
29	310.8	11.9	630	6	CD470076
30	308.8	11.8	634	6	CD471204
31	308.8	11.8	634	6	CD471217
32	308.2	11.8	639	6	CD467510
33	307.2	11.7	637	6	CD467799
34	307.2	11.7	954	7	CN842891
35	304.4	11.6	618	4	BI828553
36	300.6	11.5	634	6	CD535184
37	300.4	11.5	515	1	AL705589
38	300.2	11.5	621	6	CD470214
39	298.8	11.4	699	9	CR190735
40	298.2	11.4	618	6	CD470897
41	296.2	11.3	783	6	CD469424
42	296	11.3	446	8	AQ088761
43	293.6	11.2	765	6	CD469412
44	291.2	11.1	770	6	CD469131
45	291	11.1	777	6	CD467625

ALIGNMENTS

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ACCESSION CA455045
VERSION CA455045.1 GI:24905369
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov/
Plate: LHAM14285 row: h column: 07
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/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I; Subcloned with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

FEATURES

source

ORIGIN

OY		844	CCGAGCGGCCTGGTCATACCTGTGAGGCCCATGTGGTAAACAATGCACTGACCGCGCCGCCACATATACC	903
Db		660	CCGAGCGGCCTGGTCATACCTGTGAGGCCCATGTGGTAAACAATGCACTGACCGCGCCGCCACACAC	621
OY		904	TGTATCCTGGTCAATGTGTGTCTGTACTCTGTGGCCCTGTCTCCCTGTGCGAGATATCTTGAGT	963
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Db		560	GGAGGTTCTGTGACTTCTCTGTTTAAGTGTGCTGANTCTAGTTGGTGTAAAGCTAGATT	501
OY		1024	TCAATTAGAATGGCGGCGGCTTTTTTTAATGTGTGTTCTGTGTGGGTCCAGCCCTGGTCC	1083
Db		500	TCATTCACAGTGGCGGCTGATTTTTTTAATGTGTGTTCTGTGTGGGTCCAGCCCTGGTCC	441
OY		1084	TGCTGTGACGAGATTTCTGTGTGANTCCCGGAATATCCGCTGACACAGCTGTATCGTAGCA	1144
Db		440	TGCTGTGACGAGATTTCTGTGTGANTCCCGGAATATCCGCTGACACAGCTGTATCGTAGCA	381
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Db		380	TCCTCTCAACAGTGTGTGTTCTCTCTCTGTGTGAGCTTGCCCTTTGGCATTCAGTGGGCC	321
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ACCESSION		CN839634		
VERSION		CN839634.1	GI:47945289	
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
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		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE		1 (bases 1 to 924)		
AUTHORS		NIH-MGC http://mgi.nci.nih.gov/.		
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL		Unpublished (1999)		
COMMENT		Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rml0A07 Bethesda, MD 20892 Email: csgrabs-r@mail.nih.gov Tissue Procurement: GPCR Consortium cDNA Library Preparation: GPCR Consortium cDNA Library Arrayed By: The I.M.A.G.E.B. Consortium (ILBL)		

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRB14 row: e column: 07
 High quality sequence stop: 602.
 Location/Qualifiers

FEATURES

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/_notes="vector: pCDNA3.1; site_1: varies by clone; site_2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRRI_presV.dat"
a Note: this is a NIH_MGC Library."

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ORIGIN

Query Match	22.8%;	Score 598.2;	DB 7;	length 924;
Best Local Similarity	88.9%;	Pred. No. 4.8e-145;		
Matches 659; Conservative	0;	Mismatches 78;	Indels 4;	Gaps 1;

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Db	708	CCATCAGACCCGAGCGCTGCTGCATCTGTGTGAGCCCATCTGATACCCGCTGCCGCCGC	649
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Qy	955	TCCTGAGATGATNTTCTGTGACTTCCCTGTTTAAGTGTGCTGATTTCTGTTTGTGTGAAA	1014
Db	588	TGCTGAGATGAGGTTCTGTGACTTCCCTGTTTAAGTGTGCTGATTTCTAGTTAGTGTGAAA	529
Qy	1015	CGTCAGATTCATTACAAATGCGCTGCGCTGTTTTTTATGTGTGCTTCTCTGTGGCTCCA	1074
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Qy	1195	AGTGGGCGCTGTTTTCAGGATTCACCTGTGATTTGGAAAGCTTTATTTGTATGTGATTC	1254
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Qy	1255	TAGTTTCATTTTCTGTCCGCTTTTAAACAGAGTGTGCAACCCCATCATTTACTTCTTCG	1314
Db	288	TGTTTTGCATGTCTCTGTCTCTTAAACAGTATGTGCAACCCCATCATTTACTTCTTCG	229
Qy	1315	TGGGCTCTTTTAGCGAGCTCAAAATATGCGAATCTGAGCTGTGTTCTCAAGAGGCTTC	1374
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DEFINITION	AV731610	HTF Homo sapiens cDNA clone HTFAKD08 5', mRNA sequence.	
ACCESSION	AV731610		
VERSION	AV731610.1	GI:10849155	
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Qian, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.		
TITLE	Homo sapiens cDNA HTF clones		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Zenguan Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhanjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@hgc.sh.cn This clone is available at CHGC in Shanghai.		
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 825)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@dbp-remail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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High quality sequence stop: 561.
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ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
A Note: this is a NIH_MGC library."

ORIGIN
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RESULT 11
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VERSION CN839125.1 GI:47944780
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@dbp-remail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRB14 row: e column: 02
High quality sequence stop: 701.
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ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
A Note: this is a NIH_MGC library."

ORIGIN

Query Match 19.7%; Score 516; DB 7; Length 871;
 Best Local Similarity 87.7%; Pred. No. 1.6e-123; Indels 1; Gaps 1;
 Matches 575; Conservative 0; Mismatches 80;

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 522 GAATGACACCAATCAACGAGAGTCTTCTGCTCAAGACAGACCTGAGACTTC 581
 255 GAATGACACCAATCAACGAGAGTCTTCTGCTCAAGACAGACCTGAGACTTC 314
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 LOCUS AGENCOURT 15864292 NIH MGC 145 Homo sapiens CDNA clone
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 ACCESSION CN839765 GI:47945420
 VERSION CN839765.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 953)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@nci.nih.gov
 Tissue Procurement: GPCR Consortium
 CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
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 varies by clone; ORFs were PCR-amplified and cloned into
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 clone and include the following: 5'-EcoRV-XbaI-3',
 5'-EcoRV-XbaI-3', EcoRV (TA cloned, non-directional).
 For information about which gene each clones represents,
 please visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 19.3%; Score 504.6; DB 7; Length 953;
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DEFINITION	BS210740	
ACCESSION	BS210740	
VERSION	BS210740.1	
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SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kikka, A., Hees, V., Cotren, K., Lo, K., Offenbacher, V., Danzig, J., and Ducar, M.	
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression	
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)	
MEDLINE	21227151	
PUBMED	11329013	
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com	
FEATURES	High quality sequence stop: 456. Location/Qualifiers	
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Qy	905 GTCAATCGGTAAATGTATCTGCTGTGCGGCGCTGTGCTGCGGAGATATCTGAGAGT	964
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
11423.181 Million cell updates/sec

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 20

Total number of hits satisfying chosen parameters: 105545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1830	69.9	172939	9	AC090099 Homo sapi
4	1120	42.8	192618	2	AC020568 Homo sapi
5	1101	42.1	8622	6	AX429467 Sequence
6	1100	42.0	1697	9	BC067292 Homo sapi
7	1093	41.7	1369	6	AX647081 Sequence
8	1088	41.6	1400	6	AX299158 Sequence
9	1088	41.6	1400	6	AX549388 Sequence
10	1088	41.6	1400	9	AY042215 Homo sapi
11	969	37.0	969	6	E43450 Novel prote
12	969	37.0	969	6	AX498196 Sequence
13	918	35.1	969	6	E43451 Novel prote
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17	554	21.2	969	6	AR477200 Sequence
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DEFINITION Sequence 1 from Patent WO0234914.
ACCESSION AX429465
VERSION AX429465.1 GI:21540763
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Zhao, Q., Beasley, B.M. and Wei, M.H.
Isolated human g-protein coupled receptors, nucleic acid molecules encoding human gpcr proteins, and uses thereof
JOURNAL Patent: WO 0234914-A 1 02-MAY-2002;
PE CORP NY (US)

FEATURES

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ORIGIN

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 Direct Submission
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 Research, 320 Charles Street, Cambridge, MA 02141, USA
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 On Oct 1, 2002 this sequence version replaced gi:22726159.
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 Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

 Project Information
 Center project name: L12764
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RESULT 4
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LOCUS AC020568
DEFINITION Homo sapiens chromosome 20 clone RP11-206C1, WORKING DRAFT
SEQUENCE 24 unordered pieces.
ACCESSION AC020568
VERSION AC020568.4 GI:9280789
KEYWORDS HTG; HTGS PHASBI; HTGS DRAFT.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 192618)
 Waterston, R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 192618)
 Waterston, R.H.
 Direct Submission
 Submitted (04-JUN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Jul 19, 2000 this sequence version replaced gi:9211362.

COMMENT ----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center project name: H NH0206C01
 ----- Summary Statistics -----
 Sequencing vector: M13, 93%
 Sequencing method: plasmid, 7%
 Chemistry: Dye-Primer ET, 93% of reads
 Assembly: Dye-terminator Big Dye, 7% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 179082 bases at least Q40
 Consensus quality: 183120 bases at least Q40
 Consensus quality: 185448 bases at least Q20
 Insert size: 205000; agarose-fp
 Insert size: 190318; sum-of-contigs
 Quality coverage: 3.99 in Q20 bases; sum-of-contigs
 Quality coverage: 4.34 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 24 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1279: contig of 1279 bp in length
 * 1280 1379: gap of unknown length
 * 1380 3544: contig of 2165 bp in length
 * 3545 3644: gap of unknown length
 * 3645 5441: contig of 1797 bp in length
 * 5442 5541: gap of unknown length
 * 5542 8421: contig of 2880 bp in length
 * 8422 8521: gap of unknown length
 * 8522 10096: contig of 1575 bp in length
 * 10097 10196: gap of unknown length
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 * 17877 17976: gap of unknown length
 * 17977 21534: contig of 3558 bp in length
 * 21535 21634: gap of unknown length
 * 21635 24615: contig of 2981 bp in length
 * 24616 24715: gap of unknown length
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 * 28302 28401: gap of unknown length
 * 28402 35869: contig of 7368 bp in length
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Qy	1426	CCCTGAGACTGTGCGGAGACAGATTGAGACAGTGAAGAAACCTCTGCCCTGCAGACA	1485
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BC067292			
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DEFINITION	Homo sapiens G protein-coupled receptor MRG3, mRNA (cDNA clone		
	MG:75450 IMAGE:30383708), complete cds.		
ACCESSION	BC067292		
VERSION	BC067292.1 GI:45501076		
KEYWORDS	MG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1697)		
AUTHORS	Straussberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,		

TITLE	JOURNAL	PUBLISHED	REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK	COMMENT
12477932	2	(baaes 1 to 1697)	Strausberg, R.	Direct Submission	Submitted (12-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: Dr. Michael Brownstein CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LINL) DNA Sequencing By: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@cgsc.bc.ca	Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabhu, Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalka, Duane Smalhus, Jeff Stott, Miranda Tsai, George Yang, Jacques Schein, Asim Siddiqui, Rob Holt, Marco Marra.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAX Plate: 141 Row: m Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16876452 Location/Qualifiers 1. 1697 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:75450 IMAGE:30383708" /tissue_type="Testis" /clone_lib="NIH MGC_180" /lab_host="DH10B" /note="vector: pcmv-sPORT6.1" 1. 1697 /gene="WRGX3" /db_xref="LOCUSID:117195" /db_xref="MIM:607229" 362..1330 /gene="WRGX3" /codon_start=1 /product="G protein-coupled receptor WRGX3" /protein_id="AA67292.1" /db_xref="GI:45501077" /db_xref="LOCUSID:117195" /db_xref="MIM:607229"								

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 Matches 1300; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 7
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 LOCUS Sequence 1273 from Patent EP1270724.
 DEFINITION AX647081
 ACCESSION AX647081
 VERSION AX647081.1 GI:28800068
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 SOURCE
 ORGANISM
 Homo sapiens (human)
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 Buiakyoia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
 Guanine triphosphate-binding protein coupled receptors
 Patent: EP 1270724-A 1273 02-JAN-2003;
 National Institute of Advanced Industrial Science and Technology
 (NIAST); Center for Advanced Science and Technology Incubation, Ltd.
 (CP)
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ORIGIN

Query Match 41.7%; Score 1093; DB 6; Length 1369;
 Best Local Similarity 99.8%; Pred. No. 0;
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RESULT 8
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LOCUS Sequence 30 from Patent WO0183555.
DEFINITION AX299158
ACCESSION AX299158
VERSION AX299158.1 GI:17129065
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
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AUTHORS Anderson,D.J., Dong,X., Zylka,M., Han,S.K. and Simon,M.
TITLE Pain signaling molecules
JOURNAL Patent: NO 0183555-A 30 09-NOV-2001;
CALIFORNIA INSTITUTE OF TECHNOLOGY (US)
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VERSION AX549388.1 GI:25814004
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 673 08-AUG-2002;
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Query Match 41.6%; Score 1088; DB 6; Length 1400;
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DEFINITION Homo sapiens G protein-coupled receptor (MRGX3) gene, complete cds.
ACCESSION AY042215
VERSION AY042215.1 GI:15546065

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1400)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 2 (bases 1 to 1400)
Dong, X., Han, S., Zylka, M.J., Simon, M.I. and Anderson, D.J.
A diverse family of G-proteins expressed in specific subsets of nociceptive sensory neurons

JOURNAL Cell 106 (5), 619-632 (2001)

REFERENCE MEDLINE
PUBMED 11551509

REFERENCE 2 (bases 1 to 1400)
Dong, X., Han, S., Zylka, M.J., Simon, M.I. and Anderson, D.J.
Direct Submission

JOURNAL Submitted (19-JUN-2001) Division of Biology, 216-76, California
Institute of Technology, 1201 E. California Blvd., Pasadena, CA
91125, USA

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ORIGIN

Query Match 41.6%; Score 1088; DB 9; Length 1400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION E43450
VERSION E43450.1 GI:18627716
KEYWORDS JP 200016576-A/1.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 969)
AUTHORS Matanabe, T., Terao, S. and Matsui, H.
TITLE Novel protein G-coupled receptor protein and DNA thereof
JOURNAL Patent: JP 2000166576-A 1 20-JUN-2000;
TAKEDA CHEM IND LTD
OS Homo sapiens (human)
PN JP 2000166576-A/1
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PC A61P43/00,
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DEFINITION Sequence 19 from Patent WO242461.
ACCESSION AX498196
VERSION AX498196.1 GI:23343119
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AUTHORS Chen, R., Chu, Z. L., Dang, H. T., Lowitz, K. P. and Pride, C.
TITLE Endogenous and non-endogenous versions of human g protein-coupled
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Patent: WO 0242461-A 19 30-MAY-2002;
Arena Pharmaceuticals, Inc. (US)
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LOCUS      Novel protein G-coupled receptor protein and DNA thereof.
DEFINITION
ACCESSION      E43451
VERSION      E43451.1 GI:18627717
KEYWORDS      JP 2000166576-A/2.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 969)
AUTHORS      Watanabe,T., Terao,S. and Matsui,H.
TITLE      Novel protein G-coupled receptor protein and DNA thereof
JOURNAL      Patent: JP 2000166576-A 2 20-JUN-2000;
TAKEDA CHEM IND LTD
COMMENT      OS Homo sapiens (human)

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EN      JP 2000166576-A/2
PD      20-JUN-2000
PF      30-SEP-1999 JP 1999278116
PI      TAKUYA WATANABE, SHIZUKO TERAO, HIDEKI MATSUI
PC      C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K46/00,
PC      A61P43/00,
PC      C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,C12P21/08,PC
PC      G01N33/15,
PC      G01N33/53,G01N33/566,G01N33/577/(C12N1/21,C12R1/19),(C12N5/10,PC
PC      C12R1/91),
PC      (C12P21/02,C12R1/19),(C12P21/08,C12R1/91),C12N15/00,A61K37/02,
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ORIGIN
Query Match      35.1%; Score 918; DB 6; Length 969;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 968; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      612  GCGCTGACAGAAAGCGGCTTGTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 671
Db      121  GCGCTGACAGAAAGCGGCTTGTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy      672  GTCTCATCTACATCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
Db      181  GTCTCATCTACATCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy      732  ATATGTTGCGGTTAGGCTCATCAATATCCGACATCCCATCTCCAAATCTCAGTCT 791
Db      241  ATATGTTGCGGTTAGGCTCATCAATATCCGACATCCCATCTCCAAATCTCAGTCT 300
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1101	42.1	2618	6	ABK52823
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4	1088	41.6	1400	8	ABZ42595
5	1088	41.6	1400	8	ABZ42595
6	1088	41.6	1400	12	ADH08534
7	969	37.0	969	3	AAA29811
8	969	37.0	969	6	ABT04875
9	969	37.0	969	12	AD030080
10	966	36.9	966	12	AD044603
11	966	36.9	1683	10	ADP70583
12	918	35.1	969	3	AAA29812
13	915	35.0	966	12	ADP29104
14	915	35.0	966	12	AD044605
15	867	33.1	969	3	AAA70342
16	855	32.7	1997	10	AD018121
17	747	28.5	909	8	ACC44771
18	700	26.7	912	10	ADCI2765
19	698	26.7	769	6	ABZ35127
20	554	21.2	969	2	AAZ10068
21	546	20.9	969	2	AAZ10067

22	299	11.4	954	10	ADCI2723	Adci2723 Human GPC
23	291	11.1	291	8	ACA04716	ACA04716 cDNA enco
24	275	10.5	275	10	ACA55732	ACA55732 Human sig
25	275	10.5	275	12	AD155528	Adi55528 Human pol
26	270	10.3	1323	5	AA858260	AA858260 DNA encod
27	179	6.8	969	2	AAZ10069	AAZ10069 Human dor
28	120	4.6	964	6	AD116637	Adi16637 Human NOV
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30	120	4.6	969	2	AAZ10070	AAZ10070 Human dor
31	120	4.6	969	4	AAZ20943	AAZ20943 Human G P
32	120	4.6	969	5	AA807944	AA807944 Human CDN
33	120	4.6	969	6	AAZ27494	AAZ27494 Human G-P
34	120	4.6	969	6	ABZ42891	ABZ42891 Human GPC
35	120	4.6	969	8	ACC44772	ACC44772 Human G P
36	120	4.6	969	8	ABZ81334	ABZ81334 Human Dor
37	120	4.6	969	10	AAZ1647	AAZ1647 Human GPC
38	120	4.6	969	11	ADL96465	ADL96465 Human G P
39	120	4.6	969	12	AD030078	AD030078 Human GPC
40	120	4.6	973	4	AAK51462	AAK51462 Human pol
41	120	4.6	997	6	AD116635	Adi16635 Human NOV
42	120	4.6	997	12	ADN42289	Adn42289 Human CDN
43	120	4.6	1116	4	AAH49507	AAH49507 Human GTP
44	120	4.6	1369	10	ADC86444	ADC86444 Human GPC
45	120	4.6	2040	6	AAZ3744	AAZ3744 Human Mrg

ALIGNMENTS

RESULT 1	ABK52822	ABK52822 standard; cDNA; 2618 BP.
ID	ABK52822	
XX	ABK52822	
AC	ABK52822	
XX	27-AUG-2002 (first entry)	
DT		
XX		
DE	cDNA encoding human G-protein coupled receptor (GPCR).	
XX		
KW	Human; G-protein coupled; receptor; GPCR; human protease;	
KW	human therapeutic protein; query sequence; search; gene; se;	
KW	sequence database; non-human transgenic animal; gene therapy;	
KW	chromosome 3.	
XX		
OS	Homo sapiens.	
XX		
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FT	CDS	447..1460
FT		/*tag= a
FT		/product= "Human G-protein coupled receptor (GPCR) "
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PN	W0200234914-A1.	
XX		
PD	02-MAY-2002.	
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PF	10-OCT-2001; 2001MO-US031592.	
XX		
PR	25-OCT-2000; 2000US-00695045.	
XX		
PR	31-MAY-2001; 2001US-00867570.	
XX		
PA	(PEKE) PE CORP NY.	
XX		
FI	Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EW;	
XX		
DR	WPI; 2002-463360/49.	
XX		
DR	P-PSDB; AAU97598.	
XX		
PT	Novel isolated G-protein coupled receptor peptide useful for treating	
PT	disorder characterized by absence of, in appropriate or unwanted	
PT	expression of the receptor protein, and as immunogens to raise	
XX	antibodies.	
PS	Claim 4; Fig 1; 75pp; English.	

XX The present invention relates to a new G-protein coupled receptor (GPCR) peptide. The invention is useful for identifying a modulator of GPCR and for treating a disease or condition mediated by a human protease. The invention is also useful as models for the development of human CC therapeutics, for identifying therapeutic proteins, as targets for development of human therapeutic agents, and as query sequence to perform a search against sequence databases to, for e.g., identify other family members of related sequences. The vector of the invention is useful for producing a GPCR protein or peptide, for conducting cell-based assays involving the GPCR protein or its fragment, for identifying GPCR protein mutants whose functions are affected, and to produce non human transgenic animals. The present nucleic acid sequence represents the human G-protein coupled receptor (GPCR) gene located on chromosome 3. This sequence encodes the human G-protein coupled receptor (GPCR) protein of the invention.

SQ Sequence 2618 BP, 655 A, 637 C, 546 G, 780 T, 0 U, 0 Other;

Query Match 100.0%; Score 2618; DB 6; Length 2618;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACATTCCCGGATTTGGGACGAGATTAATCTAGTTTAAAGGCTGAGACCT 60
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DB CCTCCCTCTCTTACTCTGCTCTACCATGTGAGACGCTGCTCCCTTTGGCTT 120
QY 61 CCTCCCTCTCTTACTCTGCTCTACCATGTGAGACGCTGCTCCCTTTGGCTT 120
DB 61 CCTCCCTCTCTTACTCTGCTCTACCATGTGAGACGCTGCTCCCTTTGGCTT 120
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QY 601 TTTCCCTGTGCGCTGACAGAGAAAGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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QY 661 GCAGAGACGCTGTCTCATCTTCACTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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DB 721 GCGGCAATTAATATGTTGCGGCTTACGCTCATCAATATCCGCAATCCATCTCCAAA 780
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QY 901 ACCGTGATGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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DB 1801 CCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860

QY 1861 TCATGTTCCCTTTATGACTGAGGCAATTACTGCACTGGAAAGCTCAATTCCTTAATAGT 1920
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 RESULT 2
 ABK52823 standard; DNA; 8622 BP.
 ID ABK52823;
 AC ABK52823;
 XX 27-AUG-2002 (first entry)
 DE Genomic DNA encoding human G-protein coupled receptor (GPCR).
 XX Human; G-protein coupled; receptor; GPCR; human protease;
 XX human therapeutic protein; query sequence; search; gene; de;
 KM sequence database; non-human transgenic animal; gene therapy;
 XX chromosome 3.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 4300.8496
 FT CDS

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 FT exon
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 FT 4320.7502
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 FT 7503.8496
 FT /*tag= d
 FT /number= 2
 PN WO200234914-A1.
 XX 02-MAY-2002.
 PD 10-OCT-2001; 2001NO-US031592.
 XX 25-OCT-2000; 2000US-00695045.
 PR 31-MAY-2001; 2001US-00867570.
 XX (PEKE) PE CORP NY.
 PA Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM;
 PI WPI; 2002-463360/49.
 DR P-PSDB; AAU97598.
 XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterized by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies.
 XX Claim 4; Fig 3; 75pp; English.
 PS The present invention relates to a new G-protein coupled receptor (GPCR)
 CC peptide. The invention is useful for identifying a modulator of GPCR and
 CC for treating a disease or condition mediated by a human protease. The
 CC invention is also useful as models for the development of human
 CC therapeutic, for identifying therapeutic proteins, as targets for
 CC development of human therapeutic agents, and as query sequence to perform
 CC a search against sequence databases to, for e.g., identify other family
 CC members of related sequences. The vector of the invention is useful for
 CC producing a GPCR protein or peptide, for conducting cell-based assays
 CC involving the GPCR protein or its fragment, for identifying GPCR protein
 CC mutants whose functions are affected, and to produce non-human transgenic
 CC animals. The present nucleic acid sequence represents the human G-protein
 CC coupled receptor (GPCR) gene located on chromosome 3. This sequence
 CC encodes the human G-protein coupled receptor (GPCR) protein of the
 CC invention
 CC
 SQ Sequence 8622 BP; 2684 A; 1921 C; 1679 G; 2338 T; 0 U; 0 Other:
 Query Match 42.1%; Score 1101; DB 6; Length 8622;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 7502 GGGTCATCAGACTGGGGTTTCTGAGCATGATTCACCATCCAGTTGGGTACAGAAC 525
 QY 526 TGACACCAATCAACGAGCGTGAAGAGCTCTGCTTACAGAGACCTGAGCTTCAAGG 585
 DB 7562 TGACACCAATCAACGAGCGTGAAGAGCTCTGCTTACAGAGACCTGAGCTTCAAGG 7621
 QY 586 GGGTCATCAGACTGGGGTTTCTGAGCATGATTCACCATCCAGTTGGGTACAGAAC 645
 DB 7622 GGGTCATCAGACTGGGGTTTCTGAGCATGATTCACCATCCAGTTGGGTACAGAAC 7681
 QY 646 TGGGCTGCGCGATGCGGAGAGAGCTGTCTCAATCAATCAATCAATCAATCAATCAAT 705
 DB 7682 TGGGCTGCGCGATGCGGAGAGAGCTGTCTCAATCAATCAATCAATCAATCAATCAAT 7741

[illegible]

XX	Homo sapiens.
XX	EPI270724-A2.
XX	02-JAN-2003.
XX	18-JUN-2002; 2002EP-00013517.
XX	18-JUN-2001; 2001JP-00246789.
XX	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX	(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX	Suwa M, Asai K, Akiyama Y, Aburatani H;
XX	WPI; 2003-315783/31.
XX	P-PSDB; AD068621.
PT	New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
CC	Claim 1; SEQ ID NO 1273; 28bp; English.
CC	The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polyepitide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in AD085548-AD087616 encode GPCR's of the invention.
CC	Sequence 1369 BP; 272 A; 372 C; 340 G; 385 T; 0 U; 0 Other;
Q0	Query Match 41.7%; Score 1093; DB 10; Length 1369;
	Match Local Similarity 99.8%; Pred. No. 0;
	Matches 1193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	466 GGATCATCAGACTGGGTTTCTGACATGATTCGAACCAATCCAGCTTGAGTACAGAAC 525
Db	175 GGGTCATCAGACTGGGTTTCTGACATGATTCGAACCAATCCAGCTTGAGTACAGAAC 234
OY	526 TGACACCATTAAAGGACGTGAGAGACTCTTGTCTAACAGCACAACCTTAGCTTACCGG 585
Db	235 TGACACCATTAAAGGACGTGAGAGACTCTTGTCTAACAGCACAACCTTAGCTTACCGG 294
OY	586 GGCTGAGTGCATCGTTTCCCTTTCGCGCGTGAAGGAAACGCCGTTGTCTCGGCTCC 645
Db	295 GGCTGAGTGCATCGTTTCCCTTTCGCGCTGAAGGAAACGCCGTTGTCTCGGCTCC 354
OY	646 TGGGCTGCGCATCGCAGAGAACGCTGTTCATCATCATCTCAACCTGGTGGCGCG 705
Db	355 TGGGCTGCGCATCGCAGAGAACGCTGTTCATCATCATCTCAACCTGGTGGCGCG 414
OY	706 ACTTCTCTTCTTAAGCGGCGCACATTATATGTTGGCGTTACGGCTCATCAATAATCCGCC 765
Db	415 ACTTCTCTTCTTAAGCGGCGCACATTATATGTTGGCGTTACGGCTCATCAATAATCCGCC 474
OY	766 ATCCCATCTCCAATAATCCTGACGCTGTGATGACCTTTCCTACTTTAAGGCTTAAGCA 825
Db	475 ATCCCATCTCCAATAATCCTGACGCTGTGATGACCTTTCCTACTTTAAGGCTTAAGCA 534
OY	826 TGCTGAGGCGCATCAGCAGCGAGCGCTGCTCATCTGTGCGCATCTGTATACACT 885
Db	535 TGCTGAGGCGCATCAGCAGCGAGCGCTGCTCATCTGTGCGCATCTGTATACACT 594
OY	886 GCCGCGCGCCAGATACCTGTCAATCGGTCAATGTGTCTGTCTGTGGCCCTGTCTCCCTGC 945
Db	595 GCCGCGCGCCAGATACCTGTCAATCGGTCAATGTGTCTGTCTGTGGCCCTGTCTCCCTGC 654
OY	946 TGGGAGATATCTGAGATGATATGTTCTGTGACTTCGTGTTAAGTGTGCTCATTTCTGTTT 1005


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Db      655 TGGGAGATATCTGGAGTGAATGTTCTGTGATCTTCCGTTAGTGGTCAATATCTGTTT 714
Qy      1006 GGGTGAAGACGTAGATTTCAATTAACAATCGGAGGCGGTTTTTTTATATGAGGTTCTT 1065
Db      715 GGTGTGAAGAGTCAAGATTCAATTAACAATCGGAGGCGGTTTTTTTATATGAGGTTCTT 774
Qy      1066 GTGGGTCAAGCCTGATCTCTGCTGTGTCAGAAATTCCTGTGTGATCCCGAAGATGCGCTGA 1125
Db      775 GTGGGTCAAGCCTGATCTCTGCTGTGTCAGAAATTCCTGTGTGATCCCGAAGATGCGCTGA 834
Qy      1126 CCAAGGCTGAAGTGAACCATCTCTCTCAAGTGTGTCTTCTCTGTGGCGTGGCCCT 1185
Db      835 CCAAGGCTGAAGTGAACCATCTCTCTCAAGTGTGTCTTCTCTGTGGCGTGGCCCT 894
Qy      1186 TTGGGCAATTCAGTGGGCGGCTGTTTCCAGATCCCACTGATGTAAGAAAGTCTTATTTGTC 1245
Db      895 TTGGGCAATTCAGTGGGCGGCTGTTTCCAGATCCCACTGATGTAAGAAAGTCTTATTTGTC 954
Qy      1246 ATGTGCAATTCAGTGGGCGGCTGTTTCCAGATCCCACTGATGTAAGAAAGTCTTATTTGTC 1305
Db      955 ATGTGCAATTCAGTGGGCGGCTGTTTCCAGATCCCACTGATGTAAGAAAGTCTTATTTGTC 1014
Qy      1306 ACTTCTTCTGTGGGCTCTTGTAGGAGCGGTCAAAAATAGGAGAACTTGAAGCTGTGCTCC 1365
Db      1015 ACTTCTTCTGTGGGCTCTTGTAGGAGCGGTCAAAAATAGGAGAACTTGAAGCTGTGCTCC 1074
Qy      1366 AGAGGGCTCTGACAGAGAACCGCTGAGTGAAGTGAAGGTTGGCTTCTCTAGAGAAA 1425
Db      1075 AGAGGGCTCTGACAGAGAACCGCTGAGTGAAGTGAAGGTTGGCTTCTCTAGAGAAA 1134
Qy      1426 CCGTGAAGCTGTGGGAGAGAGATTTGAGAGAGTGAAGAGAACTTGGCCCTGTCAAGCA 1485
Db      1135 CCGTGAAGCTGTGGGAGAGAGATTTGAGAGAGTGAAGAGAACTTGGCCCTGTCAAGCA 1194
Qy      1486 GGAATTTGAGAGAAATGCTGCGCTCCGACACCTTGAACATTAATATGATTTTCTTAGCCT 1545
Db      1195 GGAATTTGAGAGAAATGCTGCGCTCCGACACCTTGAACATTAATATGATTTTCTTAGCCT 1254
Qy      1546 TCTGCTCTGAGAAATGTTCTGAGTGTGCTCTCAAGGTTCTTCAATATGATTTTATTAACCT 1605
Db      1255 TCTGCTCTGAGAAATGTTCTGAGTGTGCTCTCAAGGTTCTTCAATATGATTTTATTAACCT 1314
Qy      1606 GAGAGTTGAGGTTTCCATCCATGGAAGCAATTAATGTCAGACATCAATGTTTGA 1660
Db      1315 GAGAGTTGAGGTTTCCATCCATGGAAGCAATTAATGTCAGACATCAATGTTTGA 1369

RESULT 4
AAB33751
ID      AAB33751 standard; DNA; 1400 BP.
XX
AC      AAB33751;
XX
DT      01-JUL-2002 (first entry)
XX
DE      Human MrgX3 (mas-related gene) DNA.
XX
KW      Human; mas-related gene; G-protein coupled receptor; drg-12 protein;
KW      receptor; sensory perception; pain; analgesic; MrgX3; gene; ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      332..1300
FT      /tag= a
FT      /product= "Human MrgX3 protein"
XX
PN      WO200183555-A2.
XX
PD      08-NOV-2001.
XX
PF      04-MAY-2001; 2001WO-US014519.
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XX      04-MAY-2000; 2000US-0202027P.
PR      01-AUG-2000; 2000US-0222344P.
PR      03-NOV-2000; 2000US-00704707.
PR      19-APR-2001; 2001US-0285493P.
XX
PA      (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI      Anderson DJ, Dong X, Zylka M, Han S, Simon M;
XX
DR      WPI; 2002-171346/22.
XX
DR      P-PSDB; AAE21236.
XX
PT      Isolated polypeptide, Mrg, which is a G-protein coupled receptor and an
PT      isolated polypeptide, drg-12, which is also a receptor, useful for
PT      identifying agonists or antagonists for treating pain.
XX
PS      Disclosure; Page 128-129; 185pp; English.
XX
CC      The invention relates to Mrg (mas-related gene) protein, which is a G-
CC      protein coupled receptor and drg-12 protein, which is a receptor. The
CC      invention is useful for identifying compounds that bind to it, especially
CC      agonists or antagonists. Administration of an agent (e.g. the identified
CC      agonist) that increases the expression of Mrg in a mammal may be used for
CC      treating impaired sensory perception in a mammal, especially pain. The
CC      antagonist may also be useful for treating impaired sensory perception in
CC      a mammal. The present sequence is human MrgX3 DNA
XX
SQ      Sequence 1400 BP; 276 A; 375 C; 363 G; 386 T; 0 U; 0 Other;
XX
Query Match      41.6%; Score 1088; DB 6; Length 1400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      473 CAGATGAGGTTTCTGAGCATGATTCATCAACCATCCAGTTGGGTACAGAACTGACACC 532
Db      313 CAGATGAGGTTTCTGAGCATGATTCATCAACCATCCAGTTGGGTACAGAACTGACACC 372
Qy      533 AATCAACGAGCGTGAAGAGATCTCTGCTCAAGAGAACCTGAGCTTCAAGGAGGCTGAC 592
Db      373 AATCAACGAGCGTGAAGAGATCTCTGCTCAAGAGAACCTGAGCTTCAAGGAGGCTGAC 432
Qy      593 GTGCATGTTTCCCTTGTCCGCTGACAGAGAAAGCGGTTGTCTGTGCTCTGCTGAGCTG 652
Db      433 GTGCATGTTTCCCTTGTCCGCTGACAGAGAAAGCGGTTGTCTGTGCTCTGCTGAGCTG 492
Qy      653 CCGCATGCGAGAGAACGCTGTCTCAATCTCAATCTTCAACCTGAGCGGCGCACTTCT 712
Db      493 CCGCATGCGAGAGAACGCTGTCTCAATCTCAATCTTCAACCTGAGCGGCGCACTTCT 552
Qy      713 CTTCCTTAGCGGCGACATTAATATGTTGCGGTTACGCTCATCAATATTCGCCATCCAT 772
Db      553 CTTCCTTAGCGGCGACATTAATATGTTGCGGTTACGCTCATCAATATTCGCCATCCAT 612
Qy      773 CTCCAAAATCTCAGTCTGTGATGACCTTCCCACTTATATGAGGCTAAGATGCTGAG 832
Db      613 CTCCAAAATCTCAGTCTGTGATGACCTTCCCACTTATATGAGGCTAAGATGCTGAG 672
Qy      833 CGGCATCAGACACGAGGCTGCTGTCCATCTGTGGCCCATGTGTACACTGCGCGCG 892
Db      673 CGGCATCAGACACGAGGCTGCTGTCCATCTGTGGCCCATGTGTACACTGCGCGCG 732
Qy      893 CCCCAATACCTGTCAATGATGATGTTCTGTCTGTGGCCCTGTCTGCTGCGGAG 952
Db      733 CCCCAATACCTGTCAATGATGATGTTCTGTCTGTGGCCCTGTCTGCTGCGGAG 792
Qy      953 TATCTGAGATGATGTTCTGTGACCTCTGTTAGTGTGATGATGATGATGATGATGATGATG 1012
Db      793 TATCTGAGATGATGTTCTGTGACCTCTGTTAGTGTGATGATGATGATGATGATGATGATG 852
Qy      1013 AAGGTGATTTCAATTAACAATCGGAGCTGATTTTATATGATGATGATGATGATGATGATG 1072
Db      853 AAGGTGATTTCAATTAACAATCGGAGCTGATTTTATATGATGATGATGATGATGATGATG 912
```


QY 1133 GTACGTGACCAATCTCTCTCAAGTGTGCTTCTCTCTCTGTCGCTGCTCCCTTTGGCAT 1192
 DB 973 GTACGTGACCAATCTCTCTCAAGTGTGCTTCTCTCTCTGTCGCTGCTCCCTTTGGCAT 1032
 QY 1193 TCACATGGGCGCTTTTTCAGAGATCCACTGATTTGGAAGTCTTATTTTGCATGTGCA 1252
 DB 1033 TCAGTGGGCGCTTTTTCAGAGATCCACTGATTTGGAAGTCTTATTTTGCATGTGCA 1092
 QY 1253 TCTAGTTTCCATTTTCTCTGTCGCTCTTAAACAGAGTGCACCCCATCATTTACTTCTT 1312
 DB 1093 TCTAGTTTCCATTTTCTCTGTCGCTCTTAAACAGAGTGCACCCCATCATTTACTTCTT 1152
 QY 1313 CTGCGGCTCTTTTGAAGGAGCTGCAAAATATGCAAACTGAAAGTGTCTTCAAGAGGCT 1372
 DB 1153 CTGCGGCTCTTTTGAAGGAGCTGCAAAATATGCAAACTGAAAGTGTCTTCAAGAGGCT 1212
 QY 1373 TCTGACAGACACGCTGAGTGTGATGAAAGTGAAGGAGGCTTCTTCCAGAGAAACCTTGCA 1432
 DB 1213 TCTGACAGACACGCTGAGTGTGATGAAAGTGAAGGAGGCTTCTTCCAGAGAAACCTTGCA 1272
 QY 1433 GCTGTGCGGAAGCAGATTTGAGAGCAGTGAAGAACTTGTGCTGCTGTCAGACAGACTT 1492
 DB 1273 GCTGTGCGGAAGCAGATTTGAGAGCAGTGAAGAACTTGTGCTGCTGTCAGACAGACTT 1332
 QY 1493 GAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1552
 DB 1333 GAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1392
 QY 1553 CAGAAATG 1560
 DB 1393 CAGAAATG 1400

RESULT 7
 ID AAA29811 standard; cDNA, 969 BP.
 AC AAA29811;
 DT 18-AUG-2000 (first entry)

DE Human G protein-coupled receptor hH17213 encoding cDNA SEQ ID NO:3.
 XX Human; G protein-coupled receptor; hippocampus; diagnosis; screening;
 KM genetic disease; cellular function regulation; ss.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..969
 FT /*tag= a
 FT /product= "G protein-coupled receptor"

PN W0200020455-A1.
 XX 13-APR-2000.
 PD 30-SEP-1999; 99MO-JP005366.
 PF 01-OCT-1998; 98JP-00279535.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX Matanabe T, Terao Y, Matsui H;
 PI WPI; 2000-303747/26.
 DR P-PSDB; AAY90761.

XX Human-derived G protein-coupled protein and encoding nucleic acid, useful
 PT e.g. in determining ligands and treatment of diseases associated with
 PT dysfunction of the protein.
 XX Claim 6; Page 93-94; 97pp; Japanese.

XX The present sequence encodes a human-derived G protein-coupled protein
 CC designated hH17213, which is isolated from the human hippocampus. The G
 CC protein-coupled receptor can be used for preventing, treating and
 CC diagnosing genetic diseases associated with G protein-coupled protein.
 CC and for regulating cellular functions. The protein can be used to prevent
 CC and treat disorders associated with G protein-coupled protein gene
 CC dysfunction. It can also be used to identify G protein-coupled protein
 CC ligands and generating antibodies and antisera against the protein. It is
 CC also useful in constructing recombinant receptor protein expression
 CC systems, developing receptor-binding assay systems and screening drug
 CC candidates, and can be used as a probe in the genetic diagnosis of G
 CC protein-coupled protein disorders

XX Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other;
 SQ
 Query Match 37.0%; Score 969; DB 3; Length 969;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 492 ATGATTCACCAATCCAGTCTTGGGTACAGAACTGACCAATCAACGAGAGAG 551
 DB 1 ATGATTCACCAATCCAGTCTTGGGTACAGAACTGACCAATCAACGAGAGAG 60
 QY 552 ACTCCTGTACACAGACACCTGAGCTTACAGGAGGCTGAGTGCATGCTTCCCTGTC 611
 DB 61 ACTCCTGTACACAGACACCTGAGCTTACAGGAGGCTGAGTGCATGCTTCCCTGTC 120
 QY 612 GCGGTGACAGAAAGCGGTTGTGCTTGTGCTCTGAGCTGCTGCTGCTGCTGCTGCTGCT 671
 DB 121 GCGGTGACAGAAAGCGGTTGTGCTTGTGCTCTGAGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 672 GTTCATCTACATCTCAACCTGTGCGGCGCACTTCTCTTCTTACGCGCCACTT 731
 DB 181 GTTCATCTACATCTCAACCTGTGCGGCGCACTTCTCTTCTTACGCGCCACTT 240
 QY 732 ATATGTGCGCGCTTACGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCACT 791
 DB 241 ATATGTGCGCGCTTACGCTCATCAATATCCGCCATCCCATCTCCAAAATCTCACT 300
 QY 792 GTGATGACCTTCCCTACTTATATAGGCTTATAGGCTTATAGGCTTATAGGCTTATAG 851
 DB 301 GTGATGACCTTCCCTACTTATATAGGCTTATAGGCTTATAGGCTTATAGGCTTATAG 360
 QY 852 TGCCTGTCCATCTGTGCGCACTGTGTACACATGCGCGCGCCCAAGTATCTGTATCG 911
 DB 361 TGCCTGTCCATCTGTGCGCACTGTGTACACATGCGCGCGCCCAAGTATCTGTATCG 420
 QY 912 GTCATGTGTCTCTCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
 DB 421 GTCATGTGTCTCTCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 972 TGTGACTTCTGTATAGTGTCTGATTCGTGTTGTGTGAAACGTGAGATTTCATCA 1031
 DB 481 TGTGACTTCTGTATAGTGTCTGATTCGTGTTGTGTGAAACGTGAGATTTCATCA 540
 QY 1032 ATCGGCTGCTGCTTATATATGTGTGCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1091
 DB 541 ATCGGCTGCTGCTTATATATGTGTGCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 1092 AGGATTCCTGTGTATCCCGGAAGATGCGGCTGACACAGGCTGTAGCTGATCCATCTCTC 1151
 DB 601 AGGATTCCTGTGTATCCCGGAAGATGCGGCTGACACAGGCTGTAGCTGATCCATCTCTC 660
 QY 1152 ACAGTGTGCTTCTCTCTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
 DB 661 ACAGTGTGCTTCTCTCTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 1212 AGGATTCACCTGATGAAAGTCTTATTTTGTCAATGTGATCTAGATTTCCTG 1271
 DB 721 AGGATTCACCTGATGAAAGTCTTATTTTGTCAATGTGATCTAGATTTCCTG 780
 QY 1272 TCCGCTTTACAGACAGTGCACCCCATCATTTACTTCTGCGGCTCTTTAGGCGAG 1331

Db 781 TCGGCTTTAAACAGCAGTGCACACCCATCATTTACTTTCGAGGCTCTTTAGGAG 840
Qy 1332 CGTCAAAATAGGAGAACTGGAAGCTGTTCTCCAGAGGGCTCTGAGGACAGCCCTGAG 1391
Db 841 CGTCAAAATAGGAGAACTGGAAGCTGTTCTCCAGAGGGCTCTGAGGACAGCCCTGAG 900
Qy 1392 GTGATGAAGGTGAGAGGTGGCTTCTCAGAGAAACCTGAGCTGTGCGAGACAGATTG 1451
Db 901 GTGATGAAGGTGAGAGGTGGCTTCTCAGAGAAACCTGAGCTGTGCGAGACAGATTG 960
Qy 1452 GAGCAGTGA 1460
Db 961 GAGCAGTGA 969
RESULT 8
ABT04875
ID ABT04875 standard; cDNA; 969 BP.
XX
AC ABT04875;
XX
DT 11-OCT-2002 (first entry)
XX
DE Human G protein coupled receptor hRUP37 coding sequence.
XX
KW Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
OS Homo sapiens.
XX
PN M0200242461-A2.
XX
PD 30-MAY-2002.
XX
PF 26-NOV-2001; 2001MO-US044386.
XX
PR 27-NOV-2000; 2000US-0253404P.
PR 12-DEC-2000; 2000US-0255366P.
PR 20-FEB-2001; 2001US-0270286P.
PR 20-FEB-2001; 2001US-0270286P.
PR 06-APR-2001; 2001US-0282032P.
PR 06-APR-2001; 2001US-0282356P.
PR 06-APR-2001; 2001US-0282358P.
PR 06-APR-2001; 2001US-0282365P.
PR 14-MAY-2001; 2001US-0290917P.
PR 31-JUL-2001; 2001US-0309208P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
XX
DR WPI; 2002-566565/60.
XX
PT P-PSDB; ABJ04077.
XX
PT Novel endogenous and non-endogenous versions of G protein-coupled
PT receptor useful for identification of candidate compounds as receptor
PT agonists or antagonists for use as therapeutic agents.
XX
PS Claim 39; Page 74; 84pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC several human G-protein coupled receptors (GPCRs). These can be used in
CC the identification of candidate compounds as receptor agonists or inverse
CC agonists having applicability as therapeutic agents. The present sequence
CC is a GPCR coding sequence of the invention
XX
SO Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other;

Qy 492 ATGATTCACCAATCCCAAGTCTTGGGTACAGAACTGACACCAATCAACGAGCTGAGAG 551
Db 1 ATGATTCACCAATCCCAAGTCTTGGGTACAGAACTGACACCAATCAACGAGCTGAGAG 60
Qy 552 ACTCTTGTCTACAGACAGACCTTGAAGTTCACAGGGGTGACGTGACATCTTCCCTGTC 611
Db 61 ACTCTTGTCTACAGACAGACCTTGAAGTTCACAGGGGTGACGTGACATCTTCCCTGTC 120
Qy 612 GCGGTGACAGAAACGGGTTGTGCTTGGCTCTGGGCTGCGGCTGCGGACATGCGAGAGCT 671
Db 121 GCGGTGACAGAAACGGGTTGTGCTTGGCTCTGGGCTGCGGCTGCGGACATGCGAGAGCT 180
Qy 672 GTCTCAATTCACCAATCCCAAGTCTTGGGTACAGAACTGACACCAATCAACGAGCT 731
Db 181 GTCTCAATTCACCAATCCCAAGTCTTGGGTACAGAACTGACACCAATCAACGAGCT 240
Qy 732 ATATGTTGCGGTGAGGCTTCAATATATGCGGATTCCTTCTTCAAAATCTTCAATCT 791
Db 241 ATATGTTGCGGTGAGGCTTCAATATATGCGGATTCCTTCTTCAAAATCTTCAATCT 300
Qy 792 GTGATGACCTTTCCTACTTATAGGCTTAAGGCTGAGGCGCATCAGACCGAGCGC 851
Db 301 GTGATGACCTTTCCTACTTATAGGCTTAAGGCTGAGGCGCATCAGACCGAGCGC 360
Qy 852 TGCTGTCAATCCCTGAGCCCATCTGAGTACCACTGCGCGCCCGACAGATACCTGTCAATG 911
Db 361 TGCTGTCAATCCCTGAGCCCATCTGAGTACCACTGCGCGCCCGACAGATACCTGTCAATG 420
Qy 912 GTCATGTGTGCTGCTGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
Db 421 GTCATGTGTGCTGCTGCTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 972 TGTGACTCTCTGTTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTT 1031
Db 481 TGTGACTCTCTGTTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTT 540
Qy 1032 ATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
Db 541 ATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 1092 AGGATTCCTGAGATCCCGAAGATGCGCTGACCAAGCTGTACCTGATCCTCTCTC 1151
Db 601 AGGATTCCTGAGATCCCGAAGATGCGCTGACCAAGCTGTACCTGATCCTCTCTC 660
Qy 1152 ACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
Db 661 ACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 1212 AGGATCCACCTGAGATGGAAGTCTTATTTGTGATGTCATGATGTTTCATTTCTCTG 1271
Db 721 AGGATCCACCTGAGATGGAAGTCTTATTTGTGATGTCATGATGTTTCATTTCTCTG 780
Qy 1272 TCGGCTTTAAACAGCAGTGCACACCCATCATTTACTTCTTGTGAGGCTCTTTAGGAG 1331
Db 781 TCGGCTTTAAACAGCAGTGCACACCCATCATTTACTTCTTGTGAGGCTCTTTAGGAG 840
Qy 1332 CGTCAAAATAGGAGAACTGGAAGCTGTTCTCCAGAGGGCTCTGAGGACAGCCCTGAG 1391
Db 841 CGTCAAAATAGGAGAACTGGAAGCTGTTCTCCAGAGGGCTCTGAGGACAGCCCTGAG 900
Qy 1392 GTGATGAAGGTGAGAGGTGGCTTCTCAGAGAAACCTGAGCTGTGCGAGACAGATTG 1451
Db 901 GTGATGAAGGTGAGAGGTGGCTTCTCAGAGAAACCTGAGCTGTGCGAGACAGATTG 960
Qy 1452 GAGCAGTGA 1460
Db 961 GAGCAGTGA 969
RESULT 9
ADO30080
ID ADO30080 standard; cDNA; 969 BP.
XX

AC ADO30080;
XX 29-JUL-2004 (first entry)
XX Human GPCR MEGX3 polynucleotide, SEQ ID NO:1182.
DE
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KM transgenic mouse; neurological disorder; adrenal gland disorder;
KM colon disorder; intestinal disorder; cardiovascular disorder;
KM muscular disorder; blood disorder; immune disorder; bone disorder;
KM joint disorder; metabolic disorder; nutritive disorder; cancer;
KM kidney disorder; liver disorder; lung disorder; breast disorder;
KM ovary disorder; uterus disorder; prostate disorder; testis disorder;
KM skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KM thymus disorder; thyroid disorder; antiparkinsonian; autonomic;
KM cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KM CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KM virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KM dermatological; antitumor; antihypertensive; anorectic;
KM immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KM gene; ss.
XX
XX Homo sapiens.
XX WO200404000-A2.
XX 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,
XX Galtsen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
XX WPI; 2004-390329/36.
XX P-PSDB; ADO29705.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX
XX Claim 151, SEQ ID NO 1182; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
XX sequences at least 90% identical to the GPCR proteins and nucleic acids
XX of the invention; methods of treating, preventing or diagnosing diseases
XX associated with GPCRs of the invention; methods of screening for
XX compounds useful in the treatment of GPCR-related diseases; a transgenic
XX mouse comprising a GPCR gene or in an endogenous GPCR gene; cells derived
XX from the transgenic mice; kits comprising several mice, each of which has
XX a mutation in a different GPCR gene of the invention; and kits comprising
XX probes which hybridise to GPCR polynucleotides of the invention. The
XX invention further discloses variants of the GPCR polypeptides and vectors
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
XX be used in the diagnosis, treatment or prevention of a wide variety of
XX diseases including neurological disorders (e.g., Alzheimer's disease,
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
XX disorders of the adrenal gland; disorders of the colon or intestine
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
XX myocardial infarction); muscular disorders; blood disorders (e.g.,
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related
XX diseases); and disorders of the kidney, liver, lung, breast, ovary,

CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIP0 at
CC ftp.wipo.int/pub/published_pcf_sequences.

XX Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other;

XX Query Match 37.0%; Score 969; DB 12; Length 969;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

492 ATGATTCACACCATCCAGTCTTGAGTACAGAACTGACCAACATCAACGAGCTAGAG 551
1 ATGATTCACACCATCCAGTCTTGAGTACAGAACTGACCAACATCAACGAGCTAGAG 60
552 ACTCTTGCTACAGACCAACCTGAGCTTACAGGGGCTGAGAGTGTCTTCCCTTGTG 611
61 ACTCTTGCTACAGACCAACCTGAGCTTACAGGGGCTGAGAGTGTCTTCCCTTGTG 120
612 GCGTGAACGAGAAAGCGGTTGTGCTGAGCTCTGAGGCTGCCGATGCGAGAGAGCT 671
121 GCGTGAACGAGAAAGCGGTTGTGCTGAGCTCTGAGGCTGCCGATGCGAGAGAGCT 180
672 GTCTCCATCTACATCTCAACCTGCTGAGGCGGAGCTTCTCTTTAGCGGCACTT 731
181 GTCTCCATCTACATCTCAACCTGCTGAGGCGGAGCTTCTCTTTAGCGGCACTT 240
732 ATATGTTGGCGTTACGCGCTCATCAATATCCGCCATCCCATCTCCAAAATCTAGTCT 791
241 ATATGTTGGCGTTACGCGCTCATCAATATCCGCCATCCCATCTCCAAAATCTAGTCT 300
792 GTGATGACCTTCCCTTACCTTATAGGCTTAAAGCATGCTAGAGGCTACGACCGAGCGC 851
301 GTGATGACCTTCCCTTACCTTATAGGCTTAAAGCATGCTAGAGGCTACGACCGAGCGC 360
852 TGCCTGTCCATCTGTGAGCCCATCTGTACCACTGCGCGCGGCCCAAGATACCTGTATCG 911
361 TGCCTGTCCATCTGTGAGCCCATCTGTACCACTGCGCGCGGCCCAAGATACCTGTATCG 420
912 GTCATGTGTGCTGCTCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
421 GTCATGTGTGCTGCTCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
972 TGTGACTTCTGTTAGTGTGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1031
481 TGTGACTTCTGTTAGTGTGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540
1032 ATCGGCTGAGCTGTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1091
541 ATCGGCTGAGCTGTTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
1092 AGGATTCCTGTGATATCCCGAAGATGCGCTGACAGAGCTGTATGATGATCACTCTCTC 1151
601 AGGATTCCTGTGATATCCCGAAGATGCGCTGACAGAGCTGTATGATGATCACTCTCTC 660
1152 AAGAGTGTGTT 1211
661 AAGAGTGTGTT 720
1212 AGGATTCACCTGATGAGAAAGCTTATTTGTCATGTCATGATGATGATGATGATGATGATGATGATGATGAT 1271
721 AGGATTCACCTGATGAGAAAGCTTATTTGTCATGTCATGATGATGATGATGATGATGATGATGATGATGAT 780
1272 TCCGCTTTAAGAGAGAGCCCAACCCATCACTTCTTCTGAGGCTCTCTTAAAGGAG 1331
781 TCCGCTTTAAGAGAGAGCCCAACCCATCACTTCTTCTGAGGCTCTCTTAAAGGAG 840
1332 CGTCAAAATAGGACAACTGAGAGCTGTTCTCCAGAGGGCTGTGACAGACCGCTTGA 1391
841 CGTCAAAATAGGACAACTGAGAGCTGTTCTCCAGAGGGCTGTGACAGACCGCTTGA 900

QY 1392 GTGATGAAGAGTGGAGGCTTCTCAGAGAAACCTGAGCTGTGGAGAGAGATTG 1451
DB 901 GTGATGAAGAGTGGAGGCTTCTCAGAGAAACCTGAGCTGTGGAGAGAGATTG 960
QY 1452 GAGCAGTGA 1460
DB 961 GAGCAGTGA 969

RESULT 10
ADO44603
ID ADO44603 standard; DNA; 966 BP.
XX ADO44603;
AC ADO44603;
XX 29-JUL-2004 (first entry)
DT 29-JUL-2004 (first entry)
XX Human HIT7213 protein encoding DNA.
XX
XX HIT7213; transgenic; G protein-coupled receptor; GPCR; ophthalmological;
KM cytostatic; nephrotoxic; antiinflammatory; dermatological; analgesic;
KM vulnery; neuroprotective; human; gene; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1.966
FT CDS /tag= a
FT /product= "HIT7213"
XX MO2004039972-A1.
XX 13-MAY-2004.
XX 28-OCT-2003; 2003MO-JP013781.
XX 29-OCT-2002; 2002JP-00314141.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Kaisho Y, Watanabe T, Yasuhara Y, Mori I, Taketomi S,
XX WPI; 2004-376191/35.
XX P-PSDB; ADO44602.
XX
XX HIT7213 protein, encoded DNA and transgenic animals for clarifying
PT pathological mechanism, developing therapeutic methods and screening
PT dermatitis or remedies for related diseases e.g. cataract, cancer, and
PT dermatitis.
XX
XX Disclosure; SEQ ID NO 2; 161pp; Japanese.
XX
XX The invention relates to a non-human mammal that carries a DNA integrated
CC with a foreign HIT7213 or its mutant gene, or a part of it. The non-human
CC animal is particularly a rat. Such gene shows phenotypes of e.g. cataract
CC onset, transient skin rash and proliferation-promoting activity. The
CC foreign HIT7213 gene is a gene that encodes a G protein-coupled receptor
CC (GPCR) protein HIT7213. The protein, its encoded DNA and constructed
CC transgenic animals are useful for clarifying pathological mechanism,
CC developing therapeutic methods and screening preventives or remedies for
CC related diseases e.g. cataract, cancer, and dermatitis. The present
CC sequence represents a DNA encoding a human HIT7213 protein.
XX
XX Sequence 966 BP; 170 A; 280 C; 249 G; 267 T; 0 U; 0 Other;
SQ

Query Match 36.9%; Score 966; DB 12; Length 966;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 492 ATGATTCACACATCCAGTCTTGGGTACAGAACTGACCAATCAACGACGTGAGAG 551
DB 1 ATGATTCACACATCCAGTCTTGGGTACAGAACTGACCAATCAACGACGTGAGAG 60

QY 552 ACTCTTGTCTACAGACAGACCTTGAGCTTACAGAGGAGCTGACGTGATCGTTCCCTTGTG 611
DB 61 ACTCTTGTCTACAGACAGACCTTGAGCTTACAGAGGAGCTGACGTGATCGTTCCCTTGTG 120
QY 612 GCGCTGACAGAGAAACGGGTTGTGCTTGTGCTCTGTGGGCTGCGCATGCGCAGAAAGCT 671
DB 121 GCGCTGACAGAGAAACGGGTTGTGCTTGTGCTCTGTGGGCTGCGCATGCGCAGAAAGCT 180
QY 672 GTCCTCATCTACACCTCAACCTGATCGAGGAGGAGCTTCTCTTCTTCTTACGAGGACATT 731
DB 181 GTCCTCATCTACACCTCAACCTGATCGAGGAGGAGCTTCTCTTCTTCTTACGAGGACATT 240
QY 732 ATATGTCGCGGTACGCTCATCATATATCGGCATCCATCTCCAAATCTTCAGTCT 791
DB 241 ATATGTCGCGGTACGCTCATCATATATCGGCATCCATCTTCAAATCTTCAGTCT 300
QY 792 GTGATGACCTTTCCTTCTTATATAGGCTTATAGCATGTGAGGCGCATCAGACCGAGCGC 851
DB 301 GTGATGACCTTTCCTTCTTATATAGGCTTATAGCATGTGAGGCGCATCAGACCGAGCGC 360
QY 852 TGCGTGCATCGTGGGCGCATCTGGTACACATGCGCGCGCGCAGATACCTGTCTATG 911
DB 361 TGCGTGCATCGTGGGCGCATCTGGTACACATGCGCGCGCGCAGATACCTGTCTATG 420
QY 912 GTCATGTGTGCTCTGCTGAGGCGCTGTCCCTGCTGCGAGATATCTGAGTGTGATTC 971
DB 421 GTCATGTGTGCTCTGCTGAGGCGCTGTCCCTGCTGCGAGATATCTGAGTGTGATTC 480
QY 972 TGTGACTTCTGTTTATAGTGTGCTGATTCGTTTGTGTGAAACGTGATTTTATTACA 1031
DB 481 TGTGACTTCTGTTTATAGTGTGCTGATTCGTTTGTGTGAAACGTGATTTTATTACA 540
QY 1032 ATGCGGTGCTGATTTTATAGTGTGCTGCGTGGGCTGAGGCTGATCTGCTGATTC 1091
DB 541 ATGCGGTGCTGATTTTATAGTGTGCTGCGTGGGCTGAGGCTGATCTGCTGATTC 600
QY 1092 AGGATTCCTGTGATTCCTGAGGAGATGCGCTGACACAGGCTGTATAGTATCTCTC 1151
DB 601 AGGATTCCTGTGATTCCTGAGGAGATGCGCTGACACAGGCTGTATAGTATCTCTC 660
QY 1152 ACAGTGTGCTTCTCTCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
DB 661 ACAGTGTGCTTCTCTCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 1212 AGGATTCACCTGATTTGGAAGCTTATTTGTCATGTGATCATGTTCCATTTTCTG 1271
DB 721 AGGATTCACCTGATTTGGAAGCTTATTTGTCATGTGATCATGTTCCATTTTCTG 780
QY 1272 TCGGCTCTTAACAGAGTGCACACCCCATCATTTACTTCTGAGGCTCTCTTAAAGCAG 1331
DB 781 TCGGCTCTTAACAGAGTGCACACCCCATCATTTACTTCTGAGGCTCTCTTAAAGCAG 840
QY 1332 CGTCAAAATGAGAGAACTGAAAGTGTCTTCAGAGGCTCTGACAGACGCTGAG 1391
DB 841 CGTCAAAATGAGAGAACTGAAAGTGTCTTCAGAGGCTCTGACAGAGGCTCTGAG 900
QY 1392 GTGATTAAGTGAAGGCTGCTTCTCAGAGAAACCTGAGAGCTGTGAGAGAGATTG 1451
DB 901 GTGATTAAGTGAAGGCTGCTTCTCAGAGAAACCTGAGAGCTGTGAGAGAGATTG 960
QY 1452 GAGCAG 1457
DB 961 GAGCAG 966

RESULT 11
ADP70583
ID ADP70583 standard; DNA; 1683 BP.
XX ADP70583;
XX ADP70583;
DT 12-FEB-2004 (first entry)
XX

Orphan receptor ligand-related human protein gene SeqID206.

XX ligand: orphan receptor protein; fusion protein; fluorescent protein;
 XX cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
 XX GFPuv; Enhanced GFP; EGFP; human; gene; ds.

OS Homo sapiens.

PN MO2003071272-A1.

XX 28-AUG-2003.

XX 21-FEB-2003; 2003WO-JP001901.

XX 22-FEB-2002; 2002JP-00045728.

XX 23-JUL-2002; 2002JP-00213949.

XX 11-OCT-2002; 2002JP-00298237.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;

XX WPI; 2003-697654/66.

XX P-PSDB; ADF70481.

XX Transformation of cells with a fusion protein of an orphan receptor

XX protein with a fluorescent protein useful for identification of ligands

XX to the orphan receptor.

XX Example 4; SEQ ID NO 206; 594bp; Japanese.

XX This invention relates to a novel method of identifying ligands to an

XX orphan receptor protein which comprises transforming cells with DNA

XX encoding a fusion protein of the orphan receptor with a fluorescent

XX protein, so that the fusion protein is expressed in the cells (or cell

XX membranes isolated from them) and contacting the cells with the potential

XX ligand to be tested. A suitable fluorescent protein for incorporation in

XX the fusion protein is green fluorescent protein (GFP), for example GFP-1,

XX wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the

XX identification of ligands binding to an orphan receptor protein.

XX Sequence 1683 BP; 402 A; 438 C; 401 G; 442 T; 0 U; 0 Other;

XX Query Match 36.9%; Score 966; DB 10; Length 1683;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 492 ATGATTCACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGACGATGAGAG 551

XX 1 ATGATTCACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGACGATGAGAG 60

XX 552 ACTGCTTCAAGCAGACCCCTGAGCTTCAAGGCGCTGAGTGAATGCTTCCCTTTC 611

XX 61 ACTGCTTCAAGCAGACCCCTGAGCTTCAAGGCGCTGAGTGAATGCTTCCCTTTC 120

XX 612 GCGCTGACAGAAAGCGGTTGTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 671

XX 121 GCGCTGACAGAAAGCGGTTGTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 180

XX 672 GTCTTCATCTACATCTCAACTGCTGCGGCGGCTTCTCTTCTTCTTCTTCTTCT 731

XX 181 GTCTTCATCTACATCTCAACTGCTGCGGCGGCTTCTCTTCTTCTTCTTCTTCT 240

XX 732 ATATGTTGCGGTTAGCGCTCATCAATATCGGCATCCCATCTCCAAATCCCATGCT 791

XX 241 ATATGTTGCGGTTAGCGCTCATCAATATCGGCATCCCATCTCCAAATCCCATGCT 300

XX 792 GTATGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 851

XX 301 GTATGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360

XX 852 TGCCGTGTCATCTGTCGCGCATCTGTGACCACTGCGCGCGCCGACGATACCTGTATG 911

Db 361 TGCCGTGTCATCTGTCGCGCATCTGTGACCACTGCGCGCGCCGACGATACCTGTATG 420

Qy 912 GTATGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 971

Db 421 GTATGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 480

Qy 972 TGATGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1031

Db 481 TGATGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540

Qy 1032 ATGCGTGGCGGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1091

Db 541 ATGCGTGGCGGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600

Qy 1092 AGGATTCCTGTGATCCCGAAGATGCGGCTGACCAAGCTGTACGATGACCATCTCTC 1151

Db 601 AGGATTCCTGTGATCCCGAAGATGCGGCTGACCAAGCTGTACGATGACCATCTCTC 660

Qy 1152 ACAGTGTGCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211

Db 661 ACAGTGTGCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

Qy 1212 AGGATCCACCTGGATTTGAAAGCTTATTTGTATGATGATGATGATGATGATGATGAT 1271

Db 721 AGGATCCACCTGGATTTGAAAGCTTATTTGTATGATGATGATGATGATGATGATGAT 780

Qy 1272 TCCGCTCTTAAACAGAGTCCCAACCCCATCTTCTTCTTCTTCTTCTTCTTCTTCT 1331

Db 781 TCCGCTCTTAAACAGAGTCCCAACCCCATCTTCTTCTTCTTCTTCTTCTTCTTCT 840

Qy 1332 CGTCAAAATAGGACAGACCTGAAAGCTGTTCTCCAGAGGCTCTGACAGACAGCCCTGAG 1391

Db 841 CGTCAAAATAGGACAGACCTGAAAGCTGTTCTCCAGAGGCTCTGACAGACAGCCCTGAG 900

Qy 1392 GTGATGAAAGTGGAGGCTGCTTCTCTGAGAAACCTGAGCTGTGCGGAAGAGATTG 1451

Db 901 GTGATGAAAGTGGAGGCTGCTTCTCTGAGAAACCTGAGCTGTGCGGAAGAGATTG 960

Qy 1452 GAGCAG 1457

Db 961 GAGCAG 966

RESULT 12

AAA29812

ID AAA29812 standard; cDNA; 969 BP.

XX AAA29812;

XX 18-AUG-2000 (first entry)

XX Human G protein-coupled receptor hH77213V encoding cDNA SEQ ID NO:4.

XX Human; G protein-coupled receptor; hippocampus; diagnosis; screening;

XX genetic disease; cellular function regulation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT CDS 1..969

XX FT CDS /tag= a

XX FT CDS /product= "G protein-coupled receptor"

XX PN MO20020455-A1.

XX PD 13-APR-2000.

XX PF 30-SEP-1999; 99WO-JP005366.

XX PR 01-OCT-1998; 98JP-00279535.

XX PA (TAKE) TAKEDA CHEM IND LTD.

PI Watanabe T, Terao Y, Matsui H;
 XX WPI: 2000-303747/26.
 DR P-PSDB; AAY90762.
 XX
 PT Human-derived G protein-coupled protein and encoding nucleic acid, useful
 PT e.g. in determining ligands and treatment of diseases associated with
 XX dysfunction of the protein.
 PS Claim 6; Page 94-95; 97pp; Japanese.
 XX
 CC The present sequence encodes a human-derived G protein-coupled protein
 CC designated hHR7213V, which is isolated from the human hippocampus. The G
 CC protein-coupled receptor can be used for preventing, treating and
 CC diagnosing genetic diseases associated with G protein-coupled protein,
 CC and for regulating cellular functions. The protein can be used to prevent
 CC and treat disorders associated with G protein-coupled protein gene
 CC dysfunction. It can also be used to identify G protein-coupled protein
 CC ligands and generating antibodies and antisera against the protein. It is
 CC also useful in constructing recombinant receptor protein expression
 CC systems, developing receptor-binding assay systems and screening drug
 CC candidates, and can be used as a probe in the genetic diagnosis of G
 CC protein-coupled protein disorders
 XX
 SQ Sequence 969 BP; 172 A; 280 C; 249 G; 268 T; 0 U; 0 Other;
 Query Match 35.1%; Score 918; DB 3; Length 969;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 969; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 492 ATGATTCACACATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTAGAG 551
 DB 1 ATGATTCACACATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGTAGAG 60
 QY 552 ACTCTCTGTACAGACGACCTTGAAGCTTCAACGAGCGTAGAGCGTCTTCCCTTGTG 611
 DB 61 ACTCTCTGTACAGACGACCTTGAAGCTTCAACGAGCGTAGAGCGTCTTCCCTTGTG 120
 QY 612 GCGCTGACAGGAAACGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
 DB 121 GCGCTGACAGGAAACGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 672 GTCTCATCATCACTCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
 DB 181 GTCTCATCATCACTCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 732 ATATGTTCCGCGTTAGCGCTCATCAATATCCGCCATCCATCTTCAAAATCTTCAAGTCT 791
 DB 241 ATATGTTCCGCGTTAGCGCTCATCAATATCCGCCATCCATCTTCAAAATCTTCAAGTCT 300
 QY 792 GATGATACCTTTCCCTTATAGGCTTAAGCATGCTGAGCGGCATCAGACCGAGCGC 851
 DB 301 GATGATACCTTTCCCTTATAGGCTTAAGCATGCTGAGCGGCATCAGACCGAGCGC 360
 QY 852 TGCCGTGATCATCTGAGCGGCATCTGATCACTGAGCGGCAGCGGCAGATACCTGTCAATG 911
 DB 361 TGCCGTGATCATCTGAGCGGCATCTGATCACTGAGCGGCAGCGGCAGATACCTGTCAATG 420
 QY 912 GTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
 DB 421 GTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 972 TGTGACTTCTGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
 DB 481 TGTGACTTCTGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 1032 ATGCGGCGCGGCTTTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
 DB 541 ATGCGGCGCGGCTTTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 1092 AGGATTCCTGTGAGATCCCGAAGATGCGCTGACCAAGGCTGTACGTAACATCTCTCTC 1151
 DB 601 AGGATTCCTGTGAGATCCCGAAGATGCGCTGACCAAGGCTGTACGTAACATCTCTCTC 660

QY 1152 ACAATGCTGAGCTTCTCTCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
 DB 661 ACAATGCTGAGCTTCTCTCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 1212 AGATTCACCTGATGAGTGAAGTCTTATTTGTCATGTCATGATCTTTCATTTTCTG 1271
 DB 721 AGATTCACCTGATGAGTGAAGTCTTATTTGTCATGTCATGATCTTTCATTTTCTG 780
 QY 1272 TCCGCTCTTAAACAGACAGTGCACACCCATCATTTACTTCTTCTGAGGCTCTTTAGGAG 1331
 DB 781 TCCGCTCTTAAACAGACAGTGCACACCCATCATTTACTTCTTCTGAGGCTCTTTAGGAG 840
 QY 1332 CGTCAAAATATGGAGCAACCTGAAGCTGTTCTGACAGAGGCTGACAGACGCTGAG 1391
 DB 841 CGTCAAAATATGGAGCAACCTGAAGCTGTTCTGACAGAGGCTGACAGACGCTGAG 900
 QY 1392 GTGATGAAAGTGAAGGCTGCTTCTTCAAGAAACCTGAGAGCTGTGCGGAAAGCATTTG 1451
 DB 901 GTGATGAAAGTGAAGGCTGCTTCTTCAAGAAACCTGAGAGCTGTGCGGAAAGCATTTG 960
 QY 1452 GAGCAGTGA 1460
 DB 961 GAGCAGTGA 969
 RESULT 13
 ADF29104
 ID ADF29104 standard; cDNA; 969 BP.
 XX
 AC ADF29104;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human GPCR R-14-encoding cDNA.
 XX
 KW Human; R-14; GPCR; G protein coupled receptor;
 KW trabecular meshwork tissue; ocular outflow; antagonist;
 KW ocular hypotensive; drug screening; elevated intraocular pressure;
 KW glaucoma; ophthalmological; gene; ss.
 OS
 XX Homo sapiens.
 XX
 PN W02003080659-A1.
 PD
 XX 02-OCT-2003.
 XX
 PF 27-MAR-2003; 2003MO-CA000444.
 XX
 PR 27-MAR-2002; 2002US-0367513P.
 XX
 PA (THER-) THERATECHNOLOGIES INC.
 XX
 PI Peri KG, Mofelt S, Abrian D;
 XX
 DR WPI: 2004-053019/05.
 XX
 PT P-PSDB; ADF29105.
 XX
 PT New substantially pure R-14 polypeptide, useful as drug targets for
 PT lowering intraocular pressure and for treating condition such as
 PT glaucoma.
 XX
 PS Claim 22; SEQ ID NO 1; 85pp; English.
 XX
 CC The invention relates to a human GPCR (G protein coupled receptor)
 CC designated R-14 (ADP29105), nucleic acids encoding it (ADP29104), and R-
 CC 14 peptide antagonists (ADP29106-ADP29108). The invention also
 CC encompasses vectors and host cells comprising R-14 nucleic acids, and
 CC methods of screening for R-14 antagonists. The R-14 receptor is expressed
 CC in trabecular meshwork tissue, and is associated with a role in ocular
 CC outflow. Inhibition of the receptor results in a reduction of basal
 CC intraocular pressure, making the R-14 receptor a useful target for
 CC screening for ocular hypotensive drugs. The R-14 peptide antagonists are

CC useful for reducing intraocular pressure for the treatment of conditions
CC associated with elevated intraocular pressure such as glaucoma and
CC related conditions. The R-14 receptor, and host cells expressing an R-14
CC polynucleotide, may be used in screening for R-14 receptor antagonists.
CC The present sequence is related to the invention.

XX Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other;

Query Match 35.0%; Score 916; DB 12; Length 969;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 966; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 492 ATGATTCACCATCCAGCTTGGGTACAGAACTGACCAATCAACGAGCTGAGAG 551
DB 1 ATGATTCACCATCCAGCTTGGGTACAGAACTGACCAATCAACGAGCTGAGAG 60
QY 552 ACTGCTGCTACACAGACCCCTGAGCTTCAAGGGGCTGACGTCATGCTTCCCTTGC 611
DB 61 ACTGCTGCTACACAGACCCCTGAGCTTCAAGGGGCTGACGTCATGCTTCCCTTGC 120
QY 612 GCGCTGACAGAGAAACGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
DB 121 GCGCTGACAGAGAAACGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 672 GTCTTCATCTACATCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
DB 181 GTCTTCATCTACATCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 732 ATATGTTGCGGTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
DB 241 ATATGTTGCGGTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 792 GTGATGACCTTCCCTACTTTATAGAGCCATAGCATGCTGAGGCGCATGACGAGCGC 851
DB 301 GTGATGACCTTCCCTACTTTATAGAGCCATAGCATGCTGAGGCGCATGACGAGCGC 360
QY 852 TGCCCTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
DB 361 TGCCCTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 912 GTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
DB 421 GTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 972 TGTGATCTCTGTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
DB 481 TGTGATCTCTGTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 1032 ATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
DB 541 ATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 1092 AGGATTCCTGAGATCCCGAGAAAGTCCGCTGACAGGCTGATGAGTCAATCCCTCC 1151
DB 601 AGGATTCCTGAGATCCCGAGAAAGTCCGCTGACAGGCTGATGAGTCAATCCCTCC 660
QY 1152 ACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
DB 661 ACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 1212 AGATTCACCTGAGATGAAAGTCTTATTTGTGATGCTGATCTGATTTTCCG 1271
DB 721 AGATTCACCTGAGATGAAAGTCTTATTTGTGATGCTGATCTGATTTTCCG 780
QY 1272 TCCGCTCTTAACAGAGTGCACACCCCATCATTTACTTTGCTGAGGCTCTTTAGGCG 1331
DB 781 TCCGCTCTTAACAGAGTGCACACCCCATCATTTACTTTGCTGAGGCTCTTTAGGCG 840
QY 1332 CGTCAAAATAGGACAACTGAGTGTCTTCAGAGGCTCTGACAGACACGCTGAG 1391
DB 841 CGTCAAAATAGGACAACTGAGTGTCTTCAGAGGCTCTGACAGACACGCTGAG 900
QY 1392 GTGATGAAAGTGAAGGCTGCTTCTCTCAGAAACCTGAGAGCTGTGGGAAAGCAGATTG 1451

DB 901 GTGATGAAAGTGAAGGCTGCTTCTCAGAAACCTTGAAGCTGTGCGGAAGCAGATTG 960
QY 1452 GAGCAGT 1458
DB 961 GAGCAGT 967

RESULT 14
AD044605
ID AD044605 standard; DNA; 966 BP.

AD044605;
29-JUL-2004 (first entry)

Human H17213 protein encoding DNA.

KW H17213, transgenic; G protein-coupled receptor; GPCR; ophthalmological;
KW cytosolic; nephrotropic; antiinflammatory; dermatological; analgesic;
KW vulnery; neuroprotective; human; gene; ds.

OS Homo sapiens.

Key Location/Qualifiers
FT CDS 1..966
FT FT /*tag= a
FT FT /product= "H17213"

MO2004039972-A1.

13-MAY-2004.

28-OCT-2003; 2003WO-JP013781.

29-OCT-2002; 2002JP-00314141.

(TAKA) TAKEDA CHEM IND LTD.

Kaisho Y, Watanabe T, Yasuhara Y, Mori I, Taketomi S;

WPI: 2004-376191/35.

P-PSDB; AD044604.

PT H17213 protein, encoded DNA and transgenic animals for clarifying
PT pathological mechanism, developing therapeutic methods and screening
PT preventives or remedies for related diseases e.g. cataract, cancer, and
PT dermatitis.

PS Disclosure; SEQ ID NO 4; 161bp; Japanese.

CC The invention relates to a non-human mammal that carries a DNA integrated
CC with a foreign H17213 or its mutant gene, or a part of it. The non-human
CC animal is particularly a rat. Such gene shows phenotypes of e.g. cataract
CC onset, transient skin rash and proliferation-promoting activity. The
CC foreign H17213 gene is a gene that encodes a G protein-coupled receptor
CC (GPCR) protein H17213. The protein, its encoded DNA and constructed
CC transgenic animals are useful for clarifying pathological mechanism,
CC developing therapeutic methods and screening preventives or remedies for
CC related diseases e.g. cataract, cancer, and dermatitis. The present
CC sequence represents a DNA encoding a human H17213 protein.

XX Sequence 966 BP; 171 A; 280 C; 248 G; 267 T; 0 U; 0 Other;

Query Match 35.0%; Score 915; DB 12; Length 966;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 965; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 492 ATGATTCACCATCCAGCTTGGGTACAGAACTGACCAATCAACGAGCTGAGAG 551
DB 1 ATGATTCACCATCCAGCTTGGGTACAGAACTGACCAATCAACGAGCTGAGAG 60
QY 552 ACTGCTGCTACACAGACCCCTGAGCTTCAAGGGGCTGACGTCATGCTTCCCTTGC 611


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QY      852 TGCCTGTCATCTGTGTGCCCCATCTGTGACCACTGCCCCGCCCAAGATACCTGTGATCG 911
      |||||
Db      361 TGCCTGTCATCTGTGTGCCCCATCTGTGACCACTGCCCCGCCCAAGATACCTGTGATCG 420
QY      912 GTCAATGTGTGTCCTGTGCTGTGCCCCCTGTGCCCTGTGAGGATCTGTGAGTGTGTC 971
      |||||
Db      421 GTCAATGTGTGTCCTGTGCTGTGCCCCCTGTGCCCTGTGAGGATCTGTGAGTGTGTC 480
QY      972 TGTGACTTCTCTGTATTAGTGTGTCGATTCGTGTTGTGTGAACGTCAAGATTTCATTACA 1031
      |||||
Db      481 TGTGACTTCTCTGTATTAGTGTGTCGATTCGTGTTGTGTGAACGTCAAGATTTCATTACA 540
QY      1032 ATCGCGTGTGCTGCTTTTATGTGTGTGCTCTGTGTGAGTCCAGCTGTGCTGCTGCTC 1091
      |||||
Db      541 ATCGCGTGTGCTGCTTTTATGTGTGTGCTCTGTGTGAGTCCAGCTGTGCTGCTGCTC 600
QY      1092 AGGATTCCTGTGTGATCCCGGAAGATGCCGTGACCAAGCTGTGATGATGACATCTCTCTC 1151
      |||||
Db      601 AGGATTCCTGTGTGATCCCGGAAGATGCCGTGACCAAGCTGTGATGATGACATCTCTCTC 660
QY      1152 ACAGTGTGTGCTCTTCTCTCTCTGTGTGCTGTGCCCTTGTGCAATCAGTGTGCCCCCTGTGTTCC 1211
      |||||
Db      661 ACAGTGTGTGCTCTTCTCTCTCTGTGTGCTGTGCCCTTGTGCAATCAGTGTGCCCCCTGTGTTCC 720
QY      1212 AGGATCCACCTGTGATGTGAAGTCTTATTGTGTCAATGTGATCTAGATTTCATTTTCTG 1271
      |||||
Db      721 AGGATCCACCTGTGATGTGAAGTCTTATTGTGTCAATGTGATCTAGATTTCATTTTCTG 780
QY      1272 TCCGCTCTTAACAGCAGTGCACCAACCCCATCAATTACTTCTGTGTGAGCTCCTTTAGGCAG 1331
      |||||
Db      781 TCCGCTCTTAACAGCAGTGCACCAACCCCATCAATTACTTCTGTGTGAGCTCCTTTAGGCAG 840
QY      1332 CGTCAAAATAGGCAGAACTGTGAGTGTCTTCAGAGGGCTCTGACGAGACAGCCTGAG 1391
      |||||
Db      841 CGTCAAAATAGGCAGAACTGTGAGTGTCTTCAGAGGGCTCTGACGAGACAGCCTGAG 900
QY      1392 GTGATGAAAGTGGAGGG 1409
      |||||
Db      901 GTGATGAAAGTGGAGGG 918
      |||||
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Search completed: October 29, 2004, 19:33:33
Job time : 1232 secs

QY 865 TGTGGCCATCTGTGACCACTGCGCGCCGCCAGATACCTGTGATCGTATGTTGTC 924
DB 374 TGTGGCCATCTGTGACCACTGCGCGCCGCCAGATACCTGTGATCGTATGTTGTC 433
QY 925 TGTCTGTGGCCCTGTGCTGCTGCTGCGAGATATCTGTGATGATGTTCTGTGACTTCTGT 984
DB 434 TGTCTGTGGCCCTGTGCTGCTGCTGCGAGATATCTGTGATGATGTTCTGTGACTTCTGT 493
QY 985 TTAAGGTCGTGATCTGTGTTGTGTGTAAGCACTGATTTCAATTCAGTGGCTGTG 1044
DB 494 TTAAGTGTGTCGTGATCTGTGTTGTGTGTAAGCACTGATTTCAATTCAGTGGCTGTG 553
QY 1045 TTTTATATGTGTGTCTGTGTGTGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1104
DB 554 TTTTATATGTGTGTCTGTGTGTGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 613
QY 1105 GATCCCGGAAGATGCGCTGACAGAGCTGTGATGATCACTCTCTCAAGTGTGTCT 1164
DB 614 GATCCCGGAAGATGCGCTGACAGAGCTGTGATGATCACTCTCTCAAGTGTGTCT 673
QY 1165 TCTCTCTGTGTGCGCTGTGTGTGATTCAGTGGCCCTGTGTTTCAGATTCACCTGTG 1224
DB 674 TCTCTCTGTGTGCGCTGTGTGTGATTCAGTGGCCCTGTGTTTCAGATTCACCTGTG 733
QY 1225 ATTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCATTTTCTGTGCTGTGCTTACA 1284
DB 734 ATTGGAAGTCTTATTTTGTGATGTGATCTAGTTTCATTTTCTGTGCTGTGCTTACA 793
QY 1285 GCAGTCCCAACCCCATCATTTACTTCTTC 1313
DB 794 GCAGTCCCAACCCCATCATTTACTTCTTC 822

RESULT 2
US-09-254-227A-4
; Sequence 4, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Barville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-254-227A-4

Query Match 20.9%; Score 546; DB 4; Length 969;
Best Local Similarity 99.8%; Pred. No. 1.2e-228;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 749 CCTCATCATATCCGCCATCCCATCTCCAAAATCTCACTGTGTGATGACCTTTCCCTA 808
DB 258 CCTCATCATATCCGCCATCCCATCTCCAAAATCTCACTGTGTGATGACCTTTCCCTA 317
QY 809 CTTTATAGGCTTAAGCATGCTGAGCGCATTCAGACCGGCGCTGCTGTCTCATCTGTG 868
DB 318 CTTTATAGGCTTAAGCATGCTGAGCGCATTCAGACCGGCGCTGCTGTCTCATCTGTG 377
QY 869 GCCCATCTGTGATGACCTGCGCGCGCCGAGATACCTGTGATGATGATGATGATGATGAT 928
DB 378 GCCCATCTGTGATGACCTGCGCGCGCCGAGATACCTGTGATGATGATGATGATGATGAT 437

QY 929 CTGGGCGCTGTGCTGCTGCTGCGAGATATCTGTGATGATGATGATGATGATGATGATGAT 988
DB 438 CTGGGCGCTGTGCTGCTGCTGCGAGATATCTGTGATGATGATGATGATGATGATGATGATGAT 497
QY 989 TGTGTGTATCTGTGTTGTGTGTAAGCACTGATTTCAATTCAGTGGCTGTGACTTCTGT 1048
DB 498 TGTGTGTATCTGTGTTGTGTGTAAGCACTGATTTCAATTCAGTGGCTGTGACTTCTGT 557
QY 1049 TTTATGTGTGTTCTGTGTGTGTCAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGATC 1108
DB 558 TTTATGTGTGTTCTGTGTGTGTCAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGATC 617
QY 1109 CCGGAAGATGCGCTGACAGAGCTGTGATGATCACTCTCTCAAGTGTGTCTTCT 1168
DB 618 CCGGAAGATGCGCTGACAGAGCTGTGATGATCACTCTCTCAAGTGTGTCTTCT 677
QY 1169 CCGTGTGTGCTGCGCTGTGTGTGATTCAGTGGCCCTGTGTTTCAGATTCACCTGTGATG 1228
DB 678 CCGTGTGTGCTGCGCTGTGTGTGATTCAGTGGCCCTGTGTTTCAGATTCACCTGTGATG 737
QY 1229 GAAAGTCTTATTTTGTGATGTGATCTAGTTTCATTTTCTGTGCTGTGCTTAAACAGAG 1288
DB 738 GAAAGTCTTATTTTGTGATGTGATCTAGTTTCATTTTCTGTGCTGTGCTTAAACAGAG 797
QY 1289 TGTCAACCCCATCATTTACTTCTGTGTGCTCTTTAGGAGAGCTCAAAATAGGCA 1345
DB 798 TGTCAACCCCATCATTTACTTCTGTGTGCTCTTTAGGAGAGCTCAAAATAGGCA 854

RESULT 3
US-09-495-050A-164
; Sequence 164, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Au-Yang, Janice
; APPLICANT: Lu-Yang, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED PR
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/119,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 164
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 1909132CT1
; US-09-495-050A-164

Query Match 11.1%; Score 291; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 CGGCATCCCATCTCCAAAATCTCACTGTGTGATGACCTTTCCCTAATTTAGGCTTA 821
DB 1 CGGCATCCCATCTCCAAAATCTCACTGTGTGATGACCTTTCCCTAATTTAGGCTTA 60
QY 822 AGCATGCTGAGCGCATTCAGACCGAGGCTGCTGTCCATCTGTGCGCCATCTGTGATC 881
DB 61 AGCATGCTGAGCGCATTCAGACCGAGGCTGCTGTCCATCTGTGCGCCATCTGTGATC 120
QY 882 CACTGCGCGCGCCCAAGATACCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 941
DB 121 CACTGCGCGCGCCCAAGATACCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 942 CTGCTGCGAGATCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1001
DB 181 CTGCTGCGAGATCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

Query Match 4.6%; Score 120; DB 4; Length 969;
Best Local Similarity 100.0%; Pred. No. 9.5e-43;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1263 ATTTCTGTCGCTCTTAAACAGAGGCGCAACCCCATATTACTTCTTCTGGGCTCC 1322

DB 772 ATTTCTGTCGCTCTTAAACAGAGGCGCAACCCCATATTACTTCTTCTGGGCTCC 831

QY 1323 TTATGAGCGGCTCAAAATAGAGAGACCGTGGTCTCAGAGGGCTCGAGAGAC 1382

DB 832 TTATGAGCGGCTCAAAATAGAGAGACCGTGGTCTCAGAGGGCTCGAGAGAC 891

RESULT 7
US-09-254-227A-12
Sequence 12, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Barville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
US-09-254-227A-12

Query Match 3.7%; Score 97; DB 4; Length 969;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1287 AGTGCACCCCATATTACTTCTTCTGGGCTCTTTAGGAGAGGTCAAAATAGGAG 1346

DB 796 AGTGCACCCCATATTACTTCTTCTGGGCTCTTTAGGAGAGGTCAAAATAGGAG 855

QY 1347 AACCTGAAGCTGTTCTCAGAGGGCTCGAGAGCA 1383

DB 856 AACCTGAAGCTGTTCTCAGAGGGCTCGAGAGCA 892

RESULT 8
US-09-254-227A-14
Sequence 14, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Barville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
US-09-254-227A-14

Query Match 3.1%; Score 80; DB 4; Length 969;

Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1287 AGTGCACCCCATATTACTTCTTCTGGGCTCTTTAGGAGAGGTCAAAATAGGAG 1346

DB 796 AGTGCACCCCATATTACTTCTTCTGGGCTCTTTAGGAGAGGTCAAAATAGGAG 855

QY 1347 AACCTGAAGCTGTTCTCCA 1366

DB 856 AACCTGAAGCTGTTCTCCA 875

RESULT 9
US-09-497-855A-32/c
Sequence 32, Application US/09497855A
Patent No. 6605432
GENERAL INFORMATION:
APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REFERENCE: UMO1523
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/118,760
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
SEQ ID NO 32
LENGTH: 118067
TYPE: DNA
ORGANISM: Homo sapiens;
US-09-497-855A-32

Query Match 1.2%; Score 31; DB 4; Length 118067;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GATTGAAGCTTCTCGAGGCTCCCGCAGAG 157

DB 97535 GATTGAAGCTTCTCGAGGCTCCCGCAGAG 97505

RESULT 10
US-09-918-686-1/c
Sequence 1, Application US/09918686
Patent No. 6475739
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary
APPLICANT: Prohl, Sean
APPLICANT: Paepfer, Bryan
APPLICANT: Steahling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 92139
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7043, 8369, 8401
OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 1.1%; Score 30; DB 4; Length 92139;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GATTGGAAGCTTCTGAGGCTCCCGCAGAA 156
Db 80505 GATTGGAAGCTTCTGAGGCTCCCGCAGAA 80476

RESULT 11

US-08-871-732A-2
Sequence 2, Application US/08871732A
Patent No. 6140074
GENERAL INFORMATION:
APPLICANT: O'BRIEN, TIMOTHY J.

TITLE OF INVENTION: NOVEL SH3 PROTEIN, GENE, CHIMERIC
TITLE OF INVENTION: CELLS, VECTORS AND EXPRESSION METHOD FOR PRODUCING THE NOVEL
TITLE OF INVENTION: PROTEIN, ANTIBODIES AND USES
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: MARTIN L. MCGREGOR
STREET: 5380 WEST 34TH STREET, #345
CITY: HOUSTON
STATE: TEXAS

COUNTRY: UNITED STATES OF AMERICA
ZIP: 77092

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 3.5 INCH 1.44 MB STORAGE

COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS

SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,732A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:
NAME: MCGREGOR, MARTIN L.

REGISTRATION NUMBER: 29,329
REFERENCE/DOCKET NUMBER: 1-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-682-1213

TELEFAX: 713-682-5807
TELEX: NONE

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 735 BASE PAIRS
TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR

MOLECULE TYPE: OTHER NUCLEIC ACID
HYPOTHEetical: NO

ANTI-SENSE: NO
US-08-871-732A-2

Query Match 1.0%; Score 26; DB 3; Length 735;
Best Local Similarity 100.0%; Pred.No. 0.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2593 GTGCTGAGAAAAA 2618
Db 709 GTGCTGAGAAAAA 734

RESULT 12

US-09-346-510B-2
Sequence 2, Application US/09346510B
Patent No. 6281014
GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
FILE REFERENCE: D6221CIP

CURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: 08/871,732

PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 2
LENGTH: 735
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: cDNA sequence of TADG5 gene isolated from a cDNA

US-09-346-510B-2

Query Match 1.0%; Score 26; DB 3; Length 735;
Best Local Similarity 100.0%; Pred.No. 0.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2593 GTGCTGAGAAAAA 2618
Db 709 GTGCTGAGAAAAA 734

RESULT 13

US-07-972-481-1
Sequence 1, Application US/07972481
Patent No. 5578453
GENERAL INFORMATION:

APPLICANT: MCDONALD, PETER J

TITLE OF INVENTION: CLONING AND EXPRESSION OF TOXOPLASMA ANTIGENS AND
TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 810 GATEHOUSE ROAD

CITY: FALLS CHURCH
STATE: VIRGINIA

COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/972,481
FILING DATE: 12-Apr-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: INTERNATIONAL PCT/AU91/00347
FILING DATE: 09-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R

REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 446-102PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000

TELEFAX: (703) 205 8050
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 682 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS

LOCATION: 1..289
US-07-972-481-1

Query Match 0.9%; Score 24; DB 1; Length 682;
Best Local Similarity 100.0%; Pred.No. 0.75;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2595 GTGCTGAGAAAAA 2618

Db 650 GCTGAAAAAAAAAAAAAAAAAAAA 673

RESULT 14
US-09-149-476-179
Sequence 179, Application US/09149476

Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002p1
CURRENT APPLICATION NUMBER: US/09/149,476

EARLIER APPLICATION NUMBER: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match 0.9%; Score 24; DB 4; Length 1509;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 14560, Application US/09621976

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; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14560
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14560

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Query Match 0.9%; Score 23; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2596 CTGGAIAAAAAAAAAAAAAAAAAA 2618
DB 32 CTGGAIAAAAAAAAAAAAAAAAAA 54

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Search completed: October 30, 2004, 00:50:23
Job time : 221 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 22:34:23 ; Search time 1218 Seconds

(without alignments)
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Title: US-09-867-570-1

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Gapop 60.0 , Gapext 60.0

Searched: 3413475 seqs, 2563800928 residues

Word size : 20

Total number of hits satisfying chosen parameters: 45245

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1093	41.7	1369	15	US-10-292-798-1273
4	1088	41.6	1400	14	US-10-183-116-30
5	1088	41.6	1400	15	US-10-225-567A-673
6	969	37.0	969	9	US-09-995-225-19
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8	916	35.0	969	15	US-10-401-397A-1
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13	434	16.6	1370	15	US-10-017-161-1599	Sequence 1599, Ap
14	291	11.1	291	15	US-10-313-542-164	Sequence 164, App
15	275	10.5	275	16	US-10-305-720-330	Sequence 330, App
16	120	4.6	964	16	US-10-072-012-173	Sequence 173, App
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18	120	4.6	969	15	US-10-240-998-3	Sequence 3, App11
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24	120	4.6	969	16	US-10-072-012-171	Sequence 171, App
25	120	4.6	1369	15	US-10-017-161-1055	Sequence 1055, App
26	120	4.6	1369	15	US-10-292-798-897	Sequence 897, App
27	120	4.6	2040	14	US-10-183-116-15	Sequence 15, App1
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32	97	3.7	1604	14	US-10-183-116-32	Sequence 32, App1
33	97	3.7	1604	15	US-10-225-567A-688	Sequence 688, App
34	84	3.2	461	11	US-09-801-944B-128	Sequence 128, App
35	84	3.2	955	15	US-10-017-161-1311	Sequence 1311, App
36	84	3.2	955	15	US-10-292-798-1077	Sequence 1077, App
37	84	3.2	955	15	US-10-240-998-5	Sequence 5, App1
38	84	3.2	1005	16	US-10-072-012-177	Sequence 177, App
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40	65	2.5	966	15	US-10-240-998-9	Sequence 9, App11
41	53	2.0	966	15	US-10-240-998-6	Sequence 6, App11
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43	46	1.8	503	9	US-09-812-102-46	Sequence 46, App1
44	46	1.8	503	14	US-10-239-028-1	Sequence 1, App11
45	46	1.8	503	17	US-10-467-616-3	Sequence 3, App11

ALIGNMENTS

RESULT 1

US-09-867-570-1

Sequence 1, Application US/09867570

Publication No. US20040076951A1

GENERAL INFORMATION:

APPLICANT: MEI, Ming-Hui et al.

TITLE OR INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OR INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

FILE REFERENCE: CLO00900-CIP

CURRENT APPLICATION NUMBER: US/09/867,570

CURRENT FILING DATE: 2001-05-31

PRIOR APPLICATION NUMBER: 09/695,045

PRIOR FILING DATE: 2000-10-25

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2618

TYPE: DNA

ORGANISM: Human

US-09-867-570-1

Query Match 100.0%; Score 2618; DB 11; Length 2618;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AACATTGCCGGAATTCGACGATGAATCTAGTTGTTAAAGCTGACACT 60

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DB 61 CTTCCCTCTCTTCACTCTGCTCTCACTGATGAGAGCGCTCCCTTGGCTTT 120

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	/ Publication No. US20040076951A1	
	/ GENERAL INFORMATION:	
	/ APPLICANT: WEI, Ming-Hui et al.	
	/ TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED	
	/ TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR	
	/ FILE REFERENCE: CLO009300-CIP	
	/ CURRENT APPLICATION NUMBER: US/09/867,570	
	/ CURRENT FILING DATE: 2001-05-31	
	/ PRIOR APPLICATION NUMBER: 09/695,045	
	/ PRIOR FILING DATE: 2000-10-25	
	/ NUMBER OF SEQ ID NOS: 4	
	/ SOFTWARE: FASTSEQ for Windows Version 4.0	
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DB	7622 GGGTAGGTGATGCTTTCCCTTGTGCGCGCTGACAGAAAAGCGGTTTGTGCTTGACCTC	7681
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DB	7682 TGAGCTGCCGATGCGCAGGAACGCTGTCTCATCTACATCTTCAACTGSGTCGGGCGG	7741
QY	706 ACTTCCTCTTCTTAGCGGCAANTATATGTGCGCGTTNAGCCCTCAATAATCCGCC	765
DB	7742 ACTTCCTCTTCTTAGCGGCAANTATATGTGCGCGTTNAGCCCTCAATAATCCGCC	7801
QY	766 ATCCCATCTCAAAATCTCTAGTCTGTGATGACCTTCCCTACTTTATAGGCTTAAGCA	825
DB	7802 ATCCCATCTCAAAATCTCTAGTCTGTGATGACCTTCCCTACTTTATAGGCTTAAGCA	7861
QY	826 TGCTGAGCGCATGACGACGCGCTGCTGTCTCATTCTGTGCGCCACTTGTTACAAC	885

Db	7862	TGCTGAGCGCATAGCAGCCGAGGCGTGCCTGTGCATCTGTGGCCCATCTGTGACACT	7921
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Db	7922	GCCGCCGCCCCAGATACCTGTCAATGGATATGTGTCTGTCTGGGCCCTGTGCCCTGC	7981
Qy	946	TGCGGAGTATCTTGAGATGATGTCTGTGACTTCCCTGTTTAAGTGTGCTGATATCTGT	1005
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Qy	1066	GTGGGTCCAGCCTGTGTCTGTGTGACGAAATCTCTGTGATCCCGGAAGATGCGCTGA	1125
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Qy	1186	TTGGCATTCAGATGGGCCCTGTATTTCAGAGATCCACTGGATTGGAAAGTCTTATTTTGT	1245
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RESULT 3
US-10-292-798-1273
: Sequence 1273, Application US/10292798
: Publication NO. US20030235833A1
: GENERAL INFORMATION:
: APPLICANT: SUMA, MAKIKO
: APPLICANT: ASAI, KIYOSHI
: APPLICANT: AKIYAMA, YUTAKA
: APPLICANT: ABRATANANI, HIROFUKU
: TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
: FILE REFERENCE: 084335/166
: CURRENT APPLICATION NUMBER: US/10/292,798
: CURRENT FILING DATE: 2002-11-13
: PRIOR APPLICATION NUMBER: 10/017,161
: PRIOR FILING DATE: 2001-12-18
: PRIOR APPLICATION NUMBER: JP 2001-246789
: PRIOR FILING DATE: 2001-06-18
: NUMBER OF SEQ ID NOS: 2070
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1273
: LENGTH: 1369

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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: source
LOCATION: (1) .. (1369)
FEATURE: CDS
NAME/KEY: CDS
LOCATION: (201) .. (1169)
US-10-292-798-1273

Query Match 41.7%; Score 1093; DB 15; Length 1369;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 466 GGGTCATGAGATGGGGTTTCTGAGCATGATTCACATCCAGCTTGGGTAAGAAC 525
DB 175 GGGTCATGAGATGGGGTTTCTGAGCATGATTCACATCCAGCTTGGGTAAGAAC 234
QY 526 TGACACCAATCAACGAGCGTGAAGAGACTCTTGTCTACAGAGAACCTTGAAGCTTCAAG 585
DB 235 TGACACCAATCAACGAGCGTGAAGAGACTCTTGTCTACAGAGAACCTTGAAGCTTCAAG 294
QY 586 GGGTCATGAGATGGGGTTTCTGAGCATGATTCACATCCAGCTTGGGTAAGAAC 645
DB 295 GGGTCATGAGATGGGGTTTCTGAGCATGATTCACATCCAGCTTGGGTAAGAAC 354
QY 646 TGGGTCGCGAGATGGGAGAGAAAGCGTGTCTCATCTACATCTCAACCTGGTCCGAGCGG 705
DB 355 TGGGTCGCGAGATGGGAGAGAAAGCGTGTCTCATCTACATCTCAACCTGGTCCGAGCGG 414
QY 706 ACTTCCTCTCTTACGCGGCAATTATATGTTCGCGGTTACGCGCTCATCAATATCCGCG 765
DB 415 ACTTCCTCTCTTACGCGGCAATTATATGTTCGCGGTTACGCGCTCATCAATATCCGCG 474
QY 766 ATCCATCTCCAAATCTCTCACTGTGATGACCTTTTCCCTTATTAAGCCTTAAGCA 825
DB 475 ATCCATCTCCAAATCTCTCACTGTGATGACCTTTTCCCTTATTAAGCCTTAAGCA 534
QY 826 TGTGAGGCGCATGACGACCGAGCGCTGCTGATCTGATCTGATCTGATCTGATCTGAT 885
DB 535 TGTGAGGCGCATGACGACCGAGCGCTGCTGATCTGATCTGATCTGATCTGATCTGAT 594
QY 886 GCGCGCGCGCGAGATACCTGTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 945
DB 595 GCGCGCGCGCGAGATACCTGTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 654
QY 946 TGGGATGATCTGAGAGTGAATGTTCTGATCTGATCTGATCTGATCTGATCTGATCT 1005
DB 655 TGGGATGATCTGAGAGTGAATGTTCTGATCTGATCTGATCTGATCTGATCTGATCT 714
QY 1006 GGTGGAACGTCAGATTTTCAATTAACATGCGAGCGTGGTTTTTTTATGAGTCTCT 1065
DB 715 GGTGGAACGTCAGATTTTCAATTAACATGCGAGCGTGGTTTTTTTATGAGTCTCT 774
QY 1066 GTGGGTCCAGCGCTGTCTGTCTGATGATCTGATCTGATCTGATCTGATCTGATCT 1125
DB 775 GTGGGTCCAGCGCTGTCTGTCTGATGATCTGATCTGATCTGATCTGATCTGATCT 834
QY 1126 CGAGGCTGAGTGAATCTCTCTCAAGTGTGTTCTTCTCTCTGAGGCTGAGCTT 1185
DB 835 CGAGGCTGAGTGAATCTCTCTCAAGTGTGTTCTTCTCTCTGAGGCTGAGCTT 894
QY 1186 TTGGATTCAGTGGGCGCTTTTCAAGATGCACTGATGATGGAAGCTTATTTTGTG 1245
DB 895 TTGGATTCAGTGGGCGCTTTTCAAGATGCACTGATGATGGAAGCTTATTTTGTG 954
QY 1246 ATGTGATCTAGTTCATTTTCTGCTGCTCTTAAACAGAGTGAAGCTTAACTTAT 1305
DB 955 ATGTGATCTAGTTCATTTTCTGCTGCTCTTAAACAGAGTGAAGCTTAACTTAT 1014
QY 1306 ACTTCTTGTGGGCTCTTTAGGAGCGTCAAAATTAAGCAAGCTTAACTTATTTTCT 1365

DB 1015 ACTTCTTGTGGGCTCTTTAGGAGCGTCAAAATTAAGCAAGCTTAACTTATTTCTCC 1074
QY 1366 AGAGGCTCTGAGAGACAGCGCTGAGTGAATGAAGTGAAGGCTTCTTCAAGAA 1425
DB 1075 AGAGGCTCTGAGAGACAGCGCTGAGTGAATGAAGTGAAGGCTTCTTCAAGAA 1134
QY 1426 CCTGAGCTGTGGGAGAGAGATTTGAGAGTGAAGAGAACTTCTGCTTCAAGAA 1485
DB 1135 CCTGAGCTGTGGGAGAGAGATTTGAGAGTGAAGAGAACTTCTGCTTCAAGAA 1194
QY 1486 GAGCTTTAGAGCAATGTGCGCTGCGACCGCTTGAATTAATGATTTTCTAGCT 1545
DB 1195 GAGCTTTAGAGCAATGTGCGCTGCGACCGCTTGAATTAATGATTTTCTAGCT 1254
QY 1546 TCTGCTCAAGAAATGTCAAGTGTCTCTCAAGGCTTCAAGTGAATGATTTTCAACT 1605
DB 1255 TCTGCTCAAGAAATGTCAAGTGTCTCTCAAGGCTTCAAGTGAATGATTTTCAACT 1314
QY 1606 GAGCTTGAAGTTTCAAGCTTGAAGAGCAATTTAGTGAAGTGAAGTGAAGTGAAG 1660
DB 1315 GAGCTTGAAGTTTCAAGCTTGAAGAGCAATTTAGTGAAGTGAAGTGAAGTGAAG 1369

RESULT 4
US-10-183-116-30
Sequence 30, Application US/10183116
Publication No. US2003092035A1
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinhong
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTR 4C1CPI
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (332) ... (1297)
US-10-183-116-30

Query Match 41.6%; Score 1088; DB 14; Length 1400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 CAGACTGGGGTTTCTGAGCATGATTCACATCCAGCTTGGGTAAGAGTGAAGCAACC 532
DB 313 CAGACTGGGGTTTCTGAGCATGATTCACATCCAGCTTGGGTAAGAGTGAAGCAACC 372
QY 533 AATCAACGAGCGTGAAGAGCTCTTGTCTACAGCAACCTTGAAGCTTCAAGGCGCTGAC 592
DB 373 AATCAACGAGCGTGAAGAGCTCTTGTCTACAGCAACCTTGAAGCTTCAAGGCGCTGAC 432
QY 593 GTGATCGTTTCCCTTGTGCGGCTGACAGAGAAAGCGGTTGTGCTCTGAGGCTG 652
DB 433 GTGATCGTTTCCCTTGTGCGGCTGACAGAGAAAGCGGTTGTGCTCTGAGGCTG 492

Db 1093 TCTAGTTCATTTTCCCTGCTCGCTCTTAACAGCAGTGCACCCCATCTTACTTCTT 1152
QY 1313 CGTGGGCTCTTTAGGAGCGCGTCAAAATAGGAGAACCTGAAGCTGTTCTCCAGAGGAC 1372
Db 1153 CGTGGGCTCTTTAGGAGCGCGTCAAAATAGGAGAACCTGAAGCTGTTCTCCAGAGGAC 1212
QY 1373 TCTCAGAGACACGCTGAGTGTGATGAAGAGTGTGAGGCTGCTCTCAGAGAACCTGTGA 1432
Db 1213 TCTCAGAGACACGCTGAGTGTGATGAAGAGTGTGAGGCTGCTCTCAGAGAACCTGTGA 1272
QY 1433 GCTGTCCGGAAGCAGATTGAGAGCAGTGAAGAAACCTTGCCCTGTGACAGAGACTTT 1492
Db 1273 GCTGTCCGGAAGCAGATTGAGAGCAGTGAAGAAACCTTGCCCTGTGACAGAGACTTT 1332
QY 1493 GAGAGCAATGCGCCCTGACACCTTGAACAATATATGATTTTCTTAGCCTTGCT 1552
Db 1333 GAGAGCAATGCGCCCTGACACCTTGAACAATATATGATTTTCTTAGCCTTGCT 1392
QY 1553 CAGAAATG 1560
Db 1393 CAGAAATG 1400

RESULT 6
US-09-995-225-19
; Sequence 19, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human C
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-19

Query Match 37.0%; Score 969; DB 9; Length 969;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 ATGATTAACATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGAGAG 551
Db 1 ATGATTAACATCCAGTCTTGGGTACAGAACTGACACCAATCAACGAGCGAGAG 60
QY 552 ACTCTTGCTCAACAGACAGACCTGAGCTTCAAGGAGGCTGAGTGCATGTTTCCCTTGC 611
Db 61 ACTCTTGCTCAACAGACAGACCTGAGCTTCAAGGAGGCTGAGTGCATGTTTCCCTTGC 120
QY 612 GCGCTGAAGAGAAACGCGGTGTGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCT 671
Db 121 GCGCTGAAGAGAAACGCGGTGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 672 GTTCATCTACATCTCAACCTGGTGGCGGAGCACTTCTCTTGAAGGCGACATT 731
Db 181 GTTCATCTACATCTCAACCTGGTGGCGGAGCACTTCTCTTGAAGGCGACATT 240
QY 732 ATATGTTGCGGTTACGCGCTCATCATATCCGCGCATCTCCAAATCTCAGTCT 791
Db 241 ATATGTTGCGGTTACGCGCTCATCATATCCGCGCATCTCCAAATCTCAGTCT 300
QY 792 GTGATGACCTTTCCTTATATAGGCTTAAGCATGCTGAGCGCATCAAGACGAGCGC 851
Db 301 GTGATGACCTTTCCTTATATAGGCTTAAGCATGCTGAGCGCATCAAGACGAGCGC 360
QY 852 TGCCGTGCATCTGTCGCGCCATCTGTGACACAGTCCGCGCCAGATACCTGTCATCG 911
Db 361 TGCCGTGCATCTGTCGCGCCATCTGTGACACAGTCCGCGCCAGATACCTGTCATCG 420
QY 912 GTCATGTGTCTGCTGCTGCGCCCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
Db 421 GTCATGTGTCTGCTGCTGCGCCCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 972 TGTGATCTCTGTTTAGT 1031
Db 481 TGTGATCTCTGTTTAGT 540
QY 1032 ATCGGAGGCTGTTTAT 1091
Db 541 ATCGGAGGCTGTTTAT 600
QY 1092 AGGATTCCTGTGTATCCCGAAGATGCGCTGACAGAGCTGTACGTGACCATCTCTC 1151
Db 601 AGGATTCCTGTGTATCCCGAAGATGCGCTGACAGAGCTGTACGTGACCATCTCTC 660
QY 1152 ACAGTGCTGTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
Db 661 ACAGTGCTGTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 1212 AGGATCACTGGATTTGAAAGTCTATTGTATGATGATGATGATGATGATGATGATGAT 1271
Db 721 AGGATCACTGGATTTGAAAGTCTATTGTATGATGATGATGATGATGATGATGATGAT 780
QY 1272 TCCGCTTTAAACAGAGTGCACACCCCATATTACTTCTGCTGCTGCTGCTGCTGCTGCT 1331
Db 781 TCCGCTTTAAACAGAGTGCACACCCCATATTACTTCTGCTGCTGCTGCTGCTGCTGCT 840
QY 1332 CGTCAAAATAGGAGAACTGTAAGTGTGTCTTCCAGAGGCTGTGACAGACAGCTGAG 1391
Db 841 CGTCAAAATAGGAGAACTGTAAGTGTGTCTTCCAGAGGCTGTGACAGACAGCTGAG 900
QY 1392 GTGATGAAGGAGGAGGCTTCTCAGAGAAACCTGAGAGCTGTGAGGAGAGAGATTG 1451
Db 901 GTGATGAAGGAGGAGGCTTCTCAGAGAAACCTGAGAGCTGTGAGGAGAGAGATTG 960
QY 1452 GAGCAGTGA 1460
Db 961 GAGCAGTGA 969

OTHER INFORMATION: coding sequence for polypeptide
US-10-401-397A-1

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Query Match          35.0%; Score 916; DB 15; Length 969;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 966; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 492 ATGATTCACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGAGCGTAGAG 551
DB 1 ATGATTCACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGAGCGTAGAG 60
QY 552 ACTCTTCTTACACAGACCTTGAAGCTTCAAGGGCTGACGTGATCTTCCCTTGC 611
DB 61 ACTCTTCTTACACAGACCTTGAAGCTTCAAGGGCTGACGTGATCTTCCCTTGC 120
QY 612 GCGCTGACAGAGAAAGCGGTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
DB 121 GCGCTGACAGAGAAAGCGGTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 672 GTCTCATCTACATCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 731
DB 181 GTCTCATCTACATCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 732 ATATGTTGCGGTTACGCTCTCATCAATATCCGCAATCCCATCTCCAAATCTCA 791
DB 241 ATATGTTGCGGTTACGCTCTCATCAATATCCGCAATCCCATCTCCAAATCTCA 300
QY 792 GTGATGACCTTCCCTCACTTATAGGCTCAAGATGCTGAGCGCATCAGACCGAG 851
DB 301 GTGATGACCTTCCCTCACTTATAGGCTCAAGATGCTGAGCGCATCAGACCGAG 360
QY 852 TGCCGTGCTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 911
DB 361 TGCCGTGCTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 912 GTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
DB 421 GTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 972 TGTGATCTTCTGTTAGTGTGCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTG 1031
DB 481 TGTGATCTTCTGTTAGTGTGCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTG 540
QY 1032 ATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1091
DB 541 ATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 1092 AGGATTCCTGATGATCCCGAAGATGCGGCTGACCGAGCTGATGATCCCTGCT 1151
DB 601 AGGATTCCTGATGATCCCGAAGATGCGGCTGACCGAGCTGATGATCCCTGCT 660
QY 1152 ACAATGCTGCTCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
DB 661 ACAATGCTGCTCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 1212 AGGATTCACCTGATGATGAAAGTCTTATTTGTGATGCTGATGATGATTTCTG 1271
DB 721 AGGATTCACCTGATGATGAAAGTCTTATTTGTGATGCTGATGATGATTTCTG 780
QY 1272 TCCGCTCTTAACAGAGTGCACACCCCAATTTACTTCTGCTGCTGCTGCTGCTG 1331
DB 781 TCCGCTCTTAACAGAGTGCACACCCCAATTTACTTCTGCTGCTGCTGCTGCTG 840
QY 1332 CGTCAAAATAGGCAAGACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 1391
DB 841 CGTCAAAATAGGCAAGACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 900
QY 1392 GTGATGAGAGTGAAGGCTGCTTCTCTCAAGAAACCTGAGAGCTGCGGAAAGCA 1451
DB 901 GTGATGAGAGTGAAGGCTGCTTCTCTCAAGAAACCTGAGAGCTGCGGAAAGCA 960
QY 1452 GAGCAGT 1458
DB |||||
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DB 961 GAGCAGT 967

RESULT 9
US-10-391-074-1
; Sequence 1, Application US/10391074
; Publication No. US20040038345A1
; GENERAL INFORMATION:
; APPLICANT: Nehle, Michael
; APPLICANT: Matleier, Frank
; TITLE OF INVENTION: No. US20040038345A1e1 Human Seven-Transmembrane Receptors
; FILE REFERENCE: 7205-0008-00-000
; CURRENT APPLICATION NUMBER: US/10/391,074
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-391-074-1
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Query Match          33.1%; Score 867; DB 16; Length 969;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 492 ATGATTCACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGAGCGTAGAG 551
DB 1 ATGATTCACCATCCAGTCTTGGGTACAGAACTGACCAATCAACGAGCGTAGAG 60
QY 552 ACTCTTCTTACACAGACCTTGAAGCTTCAAGGGCTGACGTGATCTTCCCTTGC 611
DB 61 ACTCTTCTTACACAGACCTTGAAGCTTCAAGGGCTGACGTGATCTTCCCTTGC 120
QY 612 GCGCTGACAGAGAAAGCGGTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
DB 121 GCGCTGACAGAGAAAGCGGTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 672 GTCTCATCTACATCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 731
DB 181 GTCTCATCTACATCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 732 ATATGTTGCGGTTACGCTCTCATCAATATCCGCAATCCCATCTCCAAATCTCA 791
DB 241 ATATGTTGCGGTTACGCTCTCATCAATATCCGCAATCCCATCTCCAAATCTCA 300
QY 792 GTGATGACCTTCCCTCACTTATAGGCTCAAGATGCTGAGCGCATCAGACCGAG 851
DB 301 GTGATGACCTTCCCTCACTTATAGGCTCAAGATGCTGAGCGCATCAGACCGAG 360
QY 852 TGCCGTGCTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 911
DB 361 TGCCGTGCTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 912 GTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
DB 421 GTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 972 TGTGATCTTCTGTTAGTGTGCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTG 1031
DB 481 TGTGATCTTCTGTTAGTGTGCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTG 540
QY 1032 ATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1091
DB 541 ATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 1092 AGGATTCCTGATGATCCCGAAGATGCGGCTGACCGAGCTGATGATCCCTGCT 1151
DB 601 AGGATTCCTGATGATCCCGAAGATGCGGCTGACCGAGCTGATGATCCCTGCT 660
QY 1152 ACAATGCTGCTCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1211
DB 661 ACAATGCTGCTCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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QY 1212 AGATCCACCTGATGTAAGTCTTAATTTGTCATGTCATCTAGTTTCATTTCTG 1271
DB 721 AGATCCACCTGATGTAAGTCTTAATTTGTCATGTCATCTAGTTTCATTTCTG 780
QY 1272 TCCGCTCTTAACAGACAGTCCCAACCCATCTATTACTTCTTCTGCGGCTCTTTAGGAG 1331
DB 781 TCCGCTCTTAACAGACAGTCCCAACCCATCTATTACTTCTTCTGCGGCTCTTTAGGAG 840
QY 1332 CGTCAAAATAGGAGAACTGAGCTGTTCTCCAGAGGGCTCGAGAGAGCCCTGAG 1391
DB 841 CGTCAAAATAGGAGAACTGAGCTGTTCTCCAGAGGGCTCGAGAGAGCCCTGAG 900
QY 1392 GTGATGAGAGGTGAGGG 1409
DB 901 GTGATGAGAGGTGAGGG 918
RESULT 10
US-10-219-834-7
; Sequence 7, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219, 834
; PRIOR FILING DATE: 2002-08-15, 834
; PRIOR APPLICATION NUMBER: US 60/313, 658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340, 703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318, 675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355, 596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333, 417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338, 367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1997
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-219-834-7
Query Match 32.7%; Score 856; DB 14; Length 1997;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1387 CTGAGGTGATGTAAGTGAAGGTGCTCTCTCAGAAACCTGAGCTGCGGAGCA 1446
DB 1082 CTGAGGTGATGTAAGTGAAGGTGCTCTCTCAGAAACCTGAGCTGCGGAGCA 1441
QY 1447 GATTGAGCAGTGAAGAACTCTGCTCTGTCAGACAGACTTTAGAGCAATGCTGC 1506
DB 1142 GATTGAGCAGTGAAGAACTCTGCTCTGTCAGACAGACTTTAGAGCAATGCTGC 1201
QY 1507 CCGGCCACCTTGACATTTATGATCTTTCTTAGAGCTTCTGCTCAGAAATGCTCAG 1566
DB 1202 CCGGCCACCTTGACATTTATGATCTTTCTTAGAGCTTCTGCTCAGAAATGCTCAG 1261
QY 1567 TGGTCCCTCAAGGCTCTGATAGATGTTTATCTTAACCTGACAGTTTCAACCCA 1626
DB 1262 TGGTCCCTCAAGGCTCTGATAGATGTTTATCTTAACCTGACAGTTTCAACCCA 1321
QY 1627 TGGAAAGCATTAAGTCTGACAGTACATGTTTGAATTTCTCTGATATTACCAATACATTT 1686
DB 1322 TGGAAAGCATTAAGTCTGACAGTACATGTTTGAATTTCTCTGATATTACCAATACATTT 1381
QY 1687 TCCTGTATTCTGACATGATCTTTCTTACTGAACATTTTCTGACATTTTCAATGTA 1746

DB 1382 TCCCTGTATTCTGACATGATCTTTCTTCTGAAACATTTTCTGACATTTTCAATGTA 1441
QY 1747 ATAAAGAGTGTGTCGCAACAACCCATAACCTTCTTTATAGCTGTTCCATCTGAT 1806
DB 1442 ATAAAGAGTGTGTCGCAACAACCCATAACCTTCTTTATAGCTGTTCCATCTGAT 1501
QY 1807 AGTATCAAAAGAGATTCCTTATTAATCTGACATATGTTCCCTGAAATCATGT 1866
DB 1502 AGTATCAAAAGAGATTCCTTATTAATCTGACATATGTTCCCTGAAATCATGT 1561
QY 1867 TCCCTTTATGACTGAGGCAATTAATGAGTTGGAAGCTCAATTTCTTAATAGAGTTTC 1926
DB 1562 TCCCTTTATGACTGAGGCAATTAATGAGTTGGAAGCTCAATTTCTTAATAGAGTTTC 1621
QY 1927 TGTACCTCTTAATTCATTAATGATTCAGATATTAAGCAAAATTAAGACCTTAGAGAGA 1986
DB 1622 TGTACCTCTTAATTCATTAATGATTCAGATATTAAGCAAAATTAAGACCTTAGAGAGA 1681
QY 1987 GATTCTCCCTTCAATTAATAAGAGTCTTAGAATGTTTATGAATAGCCCTCTCTGTA 2046
DB 1682 GATTCTCCCTTCAATTAATAAGAGTCTTAGAATGTTTATGAATAGCCCTCTCTGTA 1741
QY 2047 TTGTCCACAGCATGTGACATGTTGGCTTGTCTAGTAAAGACATCGTGCCCT 2106
DB 1742 TTGTCCACAGCATGTGACATGTTGGCTTGTCTAGTAAAGACATCGTGCCCT 1801
QY 2107 TCCCTTGAAGACATGTAATGTTCTTATTAAGCTTCTCTGACATTAATGAATAGTGAAGA 2166
DB 1802 TCCCTTGAAGACATGTAATGTTCTTATTAAGCTTCTCTGACATTAATGAATAGTGAAGA 1861
QY 2167 GCGTATTAATATGTCACAGCATTTGATTTGCGCATTTGAAACCTCAATATTGATTTA 2226
DB 1862 GCGTATTAATATGTCACAGCATTTGATTTGCGCATTTGAAACCTCAATATTGATTTA 1921
QY 2227 AAGTGAAATTAATCTT 2242
DB 1922 AAGTGAAATTAATCTT 1937
RESULT 11
US-10-237-467-9
; Sequence 9, Application US/10237467
; Publication No. US20030186324A1
; GENERAL INFORMATION:
; APPLICANT: Liao, Jiayu
; APPLICANT: Gray, Nathanael S.
; APPLICANT: Caldwell, Jeremy C.
; APPLICANT: Schultz, Peter G.
; APPLICANT: IBM LLC
; TITLE OF INVENTION: Sensory Neuron Receptors
; FILE REFERENCE: 021288-001300US
; CURRENT APPLICATION NUMBER: US/10/237,467
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/317, 879
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR)
; OTHER INFORMATION: 7 (DRG7) (NT009307)
US-10-237-467-9
Query Match 28.5%; Score 747; DB 15; Length 909;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 847; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 612 GCGGTGACAGAAACGGGTTGTGCTGCTGCTGCGGCGGAGTGCAGAGAGGCT 671

Db 61 GCGCTGACGAAACGGGCTGTGTCTGTGCTCTGCGGCTGCCGATGCCAGAACCT 120
 Qy 672 GTCTCATCTACATCTCAACCTGTGTGCGCGGCACTTCTCTCTTACGCGGCACT 731
 Db 121 GTCTCATCTACATCTCAACCTGTGTGCGCGGCACTTCTCTCTTACGCGGCACT 180
 Qy 732 ATATGTTGCGCGGCTTACGCGCTCAATCAATCCGCAATCCCAATCCCAATCC 240
 Db 181 ATATGTTGCGCGGCTTACGCGCTCAATCAATCCGCAATCCCAATCCCAATCC 240
 Qy 792 GTGATGACCTTCCCTTATATAGGCTTACGCGGCTTACGCGGCTTACGCGGCT 851
 Db 241 GTGATGACCTTCCCTTATATAGGCTTACGCGGCTTACGCGGCTTACGCGGCT 300
 Qy 852 TGCCCTGCTCATCTGTGCGGCTTACGCGGCTTACGCGGCTTACGCGGCT 911
 Db 301 TGCCCTGCTCATCTGTGCGGCTTACGCGGCTTACGCGGCTTACGCGGCT 360
 Qy 912 GTCATGTGTGTCTGTGCGGCTTACGCGGCTTACGCGGCTTACGCGGCT 971
 Db 361 GTCATGTGTGTCTGTGCGGCTTACGCGGCTTACGCGGCTTACGCGGCT 420
 Qy 972 TGTGATCTCTGT 1031
 Db 421 TGTGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 Qy 1032 ATCCGCGGCTGT 1091
 Db 481 ATCCGCGGCTGT 540
 Qy 1092 AGAATCTCTGT 1151
 Db 541 AGAATCTCTGT 600
 Qy 1152 ACAATGCTGT 1211
 Db 601 ACAATGCTGT 660
 Qy 1212 AGAATGCTGT 1271
 Db 661 AGAATGCTGT 720
 Qy 1272 TCCGCTCTTAAACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1331
 Db 721 TCCGCTCTTAAACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 Qy 1332 CGTCAAAATAGGCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1391
 Db 781 CGTCAAAATAGGCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 Qy 1392 GTGATGAAAGT 1451
 Db 841 GTGATGAAAGT 900
 Qy 1452 GAGCAGTGA 1460
 Db 901 GAGCAGTGA 909

RESULT 12
 US-10-101-510-239
 ; Sequence 239, Application US/10101510
 ; Publication No. US20030148295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WAN, JACKSON
 ; APPLICANT: WANG, YIXIN
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 ; FILE REFERENCE: 15117.0012
 ; CURRENT APPLICATION NUMBER: US/10/101,510
 ; PRIORITY FILING DATE: 2002-03-20
 ; PRIOR FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 805

; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 239
 ; LENGTH: 769
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (750)
 ; OTHER INFORMATION: a, t, c, g, other or unknown
 US-10-101-510-239

Query Match 26.7%; Score 698; DB 15; Length 769;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 762 GCGCATCCCATCTCAAAATCTCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 821
 Db 1 GCGCATCCCATCTCAAAATCTCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
 Qy 822 AGCATGCTGAGGCGCATCAGACCGAGCGTGTGTGTGTGTGTGTGTGTGTGTGT 881
 Db 61 AGCATGCTGAGGCGCATCAGACCGAGCGTGTGTGTGTGTGTGTGTGTGTGTGT 120
 Qy 882 CACTGCGCGCGCGCGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 941
 Db 121 CACTGCGCGCGCGCGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
 Qy 942 CTGCTGCGGAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1001
 Db 181 CTGCTGCGGAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 Qy 1002 GTTGTGTGTGAACGTCAGATTTCAATTCAGTGTGTGTGTGTGTGTGTGTGTGT 1061
 Db 241 GTTGTGTGTGAACGTCAGATTTCAATTCAGTGTGTGTGTGTGTGTGTGTGTGT 300
 Qy 1062 CTGT 1121
 Db 301 CTGT 360
 Qy 1122 CTGACGAGGCTGT 1181
 Db 361 CTGACGAGGCTGT 420
 Qy 1182 CCGTTGTGCAATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1241
 Db 421 CCGTTGTGCAATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 Qy 1242 TGTCAATGT 1301
 Db 481 TGTCAATGT 540
 Qy 1302 ATTTCCTCTGT 1361
 Db 541 ATTTCCTCTGT 600
 Qy 1362 CTCAGAGGCGCTGT 1421
 Db 601 CTCAGAGGCGCTGT 660
 Qy 1422 GAAACCTGT 1481
 Db 661 GAAACCTGT 720
 Qy 1482 GACGAGCTTGT 1541
 Db 721 GACGAGCTTGT 780

RESULT 13
 US-10-017-161-1599
 ; Sequence 1599, Application US/10017161
 ; Publication No. US2003014368A1
 ; GENERAL INFORMATION:

APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABE, RYUNARI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIORITY FILING DATE: 2001-06-18
PRIORITY FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1599
LENGTH: 1370
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(1370)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(619)
FEATURE:
NAME/KEY: CDS
LOCATION: (996)..(1170)
US-10-017-161-1599

Query Match 16.6%; Score 434; DB 15; Length 1370;
Best Local Similarity 100.0%; Pred. No. 1.2e-210;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1237 TGAAGTCTTATTTTTCATGTCATCTGTTTCCATTTTCCTGTCGCTTAAAGC 996
1287 AGTGCACCCCATCATTTTCTTCTGTCGCTTCTTAAAGCAGCTTAAAGCAG 1346
997 AGTGCACCCCATCATTTTCTTCTGTCGCTTCTTAAAGCAGCTTAAAGCAG 1096
1347 AACCTGAAGTGTCTTCTGTCGAGGCTCTGTCGAGCAGCTTAAAGCAG 1406
1057 AACCTGAAGTGTCTTCTGTCGAGGCTCTGTCGAGCAGCTTAAAGCAG 1116
1407 GGGTGGCTTCTCTGAGAACCTGTCGAGGCTCTGTCGAGCAGCTTAAAGCAG 1466
1117 GGGTGGCTTCTCTGAGAACCTGTCGAGGCTCTGTCGAGCAGCTTAAAGCAG 1176
1467 ACCTGCTCCCTGTCAGACAGGCTTGAAGCAGTGTGCTGCTTGAAGCAGT 1526
1177 ACCTGCTCCCTGTCAGACAGGCTTGAAGCAGTGTGCTGCTTGAAGCAGT 1236
1527 TATGATTTTCTTGAAGCTTCTGTCGAGAACCTGTCGAGGCTTCTGAG 1586
1237 TATGATTTTCTTGAAGCTTCTGTCGAGAACCTGTCGAGGCTTCTGAG 1296
1587 ATGATTTTCTTGAAGCTTCTGTCGAGAACCTGTCGAGGCTTCTGAG 1646
1297 ATGATTTTCTTGAAGCTTCTGTCGAGAACCTGTCGAGGCTTCTGAG 1356
1647 GTACATGTTTGA 1660
1357 GTACATGTTTGA 1370

RESULT 14
US-10-313-542-164
Sequence 164, Application US/10313542
Publication No. US20030120057A1
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F

FILE REFERENCE: PA-0013 US
CURRENT APPLICATION NUMBER: US/10/313,542
CURRENT FILING DATE: 2002-12-05
PRIORITY FILING DATE: 2000-01-31
PRIORITY FILING DATE: 2000-01-31
PRIORITY FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 164
LENGTH: 291
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030120057A1 1909132CT1
US-10-313-542-164

Query Match 11.1%; Score 291; DB 15; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.5e-137;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

762 CGCCATCCATCTCCAAATCTGATCTGTGATGACCTTTCCCTTATAGGCTTA 821
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822 AGCATCTGAGGCGCCATCCAGACGAGCGCTGCTGTCATCTGTCGAGCCTGATC 881
61 AGCATCTGAGGCGCCATCCAGACGAGCGCTGCTGTCATCTGTCGAGCCTGATC 120
882 CACTGCGCGCGCCAGATCTGTCATCTGTCATCTGTCGTCGTCGTCGTCGTC 941
121 CACTGCGCGCGCCAGATCTGTCATCTGTCATCTGTCGTCGTCGTCGTCGTC 180
942 CTCTGCGAGATCTGTCGAGGATCTGTCGATCTGTCGATCTGTCGATCTGTC 1001
181 CTCTGCGAGATCTGTCGAGGATCTGTCGATCTGTCGATCTGTCGATCTGTC 240
1002 GTTGTGTCGAGATCTGTCGAGGATCTGTCGATCTGTCGATCTGTCGATCTG 1052
241 GTTGTGTCGAGATCTGTCGAGGATCTGTCGATCTGTCGATCTGTCGATCTG 291

RESULT 15
US-10-305-720-330
Sequence 330, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIORITY FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 330
LENGTH: 275
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040010136A1 1909132
US-10-305-720-330

Query Match 10.5%; Score 275; DB 16; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.3e-129;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
762 CGCCATCCATCTCCAAATCTGATCTGTGATGACCTTTCCCTTATAGGCTTA 821
1 CGCCATCCATCTCCAAATCTGATCTGTGATGACCTTTCCCTTATAGGCTTA 60

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1298	49.6	1453	32	US-09-721-588-4370	Sequence 4370, Ap
5	1147	43.8	1557	27	US-09-634-754C-740	Sequence 740, App
6	1147	43.8	1557	27	US-09-634-754C-740	Sequence 740, App
7	1147	43.8	1557	27	US-09-634-754C-740	Sequence 740, App
8	1147	43.8	1557	27	US-10-745-444-740	Sequence 740, App
9	1146	43.8	1146	23	US-09-533-367-55	Sequence 55, Appli
10	1101	42.1	8622	36	US-09-867-570-3	Sequence 3, Appli
11	1098	41.9	3988	85	US-60-201-715-47	Sequence 47, Appli
12	1093	41.7	1369	50	US-10-292-798-1273	Sequence 1273, Ap
13	1088	41.6	1400	35	PCT-US01-14519-30	Sequence 30, Appli
14	1088	41.6	1400	35	PCT-US01-14519-30	Sequence 30, Appli
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18	1088	41.6	1400	35	PCT-US01-14519-30	Sequence 30, Appli
19	1016	38.8	2068	86	US-60-212-655-228	Sequence 228, App
20	976	37.3	1136	83	US-60-185-377-107	Sequence 107, App
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22	976	37.3	1136	83	US-60-185-377-107	Sequence 107, App
23	976	37.3	1136	83	US-60-185-377-107	Sequence 107, App
24	976	37.3	1136	83	US-60-185-377-107	Sequence 107, App
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26	976	37.3	1136	83	US-60-185-377-107	Sequence 107, App
27	976	37.3	1136	83	US-60-185-377-107	Sequence 107, App
28	969	37.0	969	33	US-09-787-879C-3	Sequence 3, Appli
29	969	37.0	969	33	US-09-787-879C-3	Sequence 3, Appli
30	969	37.0	969	33	US-09-787-879C-3	Sequence 3, Appli
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34	966	36.9	1683	55	US-10-505-486-206	Sequence 206, App
35	920	35.1	920	19	US-09-343-168-309	Sequence 309, App
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37	918	35.1	969	33	US-09-787-879A-4	Sequence 4, Appli
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41	905	34.6	1011	26	US-60-302-655-9	Sequence 9, Appli
42	867	33.1	969	52	US-09-477-620A-1	Sequence 1, Appli
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44	856	32.7	1997	2	PCT-US02-36017-7	Sequence 7, Appli
45	856	32.7	1997	49	US-10-219-834-7	Sequence 7, Appli

ALIGNMENTS

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; APPLICANT: WEI, Ming-hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1000900-CIP
; CURRENT APPLICATION NUMBER: US/09/867,570
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/695,045
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: Human
US-09-867-570-1

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Query Match	100.0%	Score 2618	DB 36	Length 2618
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2618	Conservative	0	Mismatches 0	Indels 0
			Gaps 0	
1 AACAAATGCGCGAATTCGCGACGAGATGATAGTGTGTTAAAGCGTAGACACT				60
1 AACAAATGCGCGAATTCGCGACGAGATGATAGTGTGTTAAAGCGTAGACACT				60
61 CCTCCCTCTCTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT				120
61 CCTCCCTCTCTTACT				120
121 CACGAGATGGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT				180
121 CACGAGATGGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT				180
121 CACGAGATGGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT				180
181 CAGTCTGAGAGCTTATGAGCAGTAAATTCCTTCAATTTCCAGTCTCAGG				240
181 CAGTCTGAGAGCTTATGAGCAGTAAATTCCTTCAATTTCCAGTCTCAGG				240
241 TATTTCTTTTGAATTTGAGATGAACTAATACACAGACAGAGAGCAGAGATGGA				300
241 TATTTCTTTTGAATTTGAGATGAACTAATACACAGACAGAGAGCAGAGATGGA				300
301 ATCCCAAGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT				360
301 ATCCCAAGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT				360
361 TCCACCAAGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT				420
361 TCCACCAAGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT				420
421 TGGAGTGTCAACAGAGATTAAGAGATGAAAGCAATTCCTCATGCTCATGCTG				480
421 TGGAGTGTCAACAGAGATTAAGAGATGAAAGCAATTCCTCATGCTCATGCTG				480
481 GGTTCCTGAGCATGATTCACCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTG				540
481 GGTTCCTGAGCATGATTCACCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTG				540
541 GACGTGAGAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT				600
541 GACGTGAGAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT				600
601 TTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG				660
601 TTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG				660
661 GAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT				720
661 GAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT				720
721 GCGGCAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG				780
721 GCGGCAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG				780

RESULT 1
US-09-867-570-1
Sequence 1, Application US/09867570
GENERAL INFORMATION:

Qy	781	TCCTCAGGCTCCGTATGACCTTTTCCCACTTTAATAGGCTTAAGGATGCTGAGGCGCATCA	840
Dp	781	TCTCTAGCTCCGTATAGACCTTTTCCCTCACTTTAATAGGCTTAAGGATGCTGAGGCGCATCA	840
Qy	841	GCACCGAGCGCTGCTGTCATCCCTGATGGCCCATCTGATGACCATGCGCGCCAGAT	900
Dp	841	GCACCGAGCGCTGCTGTCATCCCTGATGGCCCATCTGATGACCATGCGCGCCAGAT	900
Qy	901	ACCTGTCACTGGATCAATGTGTCTGTCTGAGGCGCTGTCCCTGTGCGAGATACCTGG	960
Dp	901	ACCTGTCACTGGATCAATGTGTCTGTCTGAGGCGCTGTCCCTGTGCGAGATACCTGG	960
Qy	961	AGTGGAGTTCGTGACCTTCTCTGTATAGTGTGCTGATTCGTGTTGTGTGAAACGTGAC	1020
Dp	961	AGTGGAGTTCGTGACCTTCTCTGTATAGTGTGCTGATTCGTGTTGTGTGAAACGTGAC	1020
Qy	1021	ATTTCATTTACAAATCGCGCTGGCTGGTTTTTTTATGTGTGTTCTCTGTGGGCTCAGCCTGG	1080
Dp	1021	ATTTCATTTACAAATCGCGCTGGCTGGTTTTTTTATGTGTGTTCTCTGTGGGCTCAGCCTGG	1080
Qy	1081	TCCTGTGTGGTCAAGATTCCTGTGTGATCCGGAAGATGCGCTGACACAGCGTGTACGTGA	1140
Dp	1081	TCCTGTGTGGTCAAGATTCCTGTGTGATCCGGAAGATGCGCTGACACAGCGTGTACGTGA	1140
Qy	1141	CCATTCCTCTCAACATGTGGTCTTCTCTCTGTGTGCGCTGTGGCATTTGACATGATGAGG	1200
Dp	1141	CCATTCCTCTCAACATGTGGTCTTCTCTCTGTGTGCGCTGTGGCATTTGACATGATGAGG	1200
Qy	1201	CCCTGTTTTCCAGGATCCACCGTGAATGGAAGAATCTAATTTTGTCAATGTGATCTAATTT	1260
Dp	1201	CCCTGTTTTCCAGGATCCACCGTGAATGGAAGAATCTAATTTTGTCAATGTGATCTAATTT	1260
Qy	1261	CCATTTTTCTGTCCGCTCTTAAACAGCAGTGCACAACCCCATATTTACTTTCTTGTGGGCT	1320
Dp	1261	CCATTTTTCTGTCCGCTCTTAAACAGCAGTGCACAACCCCATATTTACTTTCTTGTGGGCT	1320
Qy	1321	CCTTTAGGCAAGCTTCAAAATATGAGCAAACTGGAAGCTGTCTCCAGAGGCGCTGTGACAGG	1380
Dp	1321	CCTTTAGGCAAGCTTCAAAATATGAGCAAACTGGAAGCTGTCTCCAGAGGCGCTGTGACAGG	1380
Qy	1381	ACAGCGCTGAAGTGAATGAAGTGAAGGATGGCTCCCTCAGAGAAACCTGAGCGTGTCCG	1440
Dp	1381	ACAGCGCTGAAGTGAATGAAGTGAAGGATGGCTCCCTCAGAGAAACCTGAGCGTGTCCG	1440
Qy	1441	GAACGAGATTGAGCAAGTGAAGAAAGAACTGTGCGCTGTGACAGCAGACTTTGAGAGCA	1500
Dp	1441	GAACGAGATTGAGCAAGTGAAGAAAGAACTGTGCGCTGTGACAGCAGACTTTGAGAGCA	1500
Qy	1501	TGCTGCCCTGCACCCCTTGAACAATTATATATATATATATATATATATATATATATATAT	1560
Dp	1501	TGCTGCCCTGCACCCCTTGAACAATTATATATATATATATATATATATATATATATATAT	1560
Qy	1561	TCTCAGTGTCCCTCAAGTCTTGGAAATGTTTATCTAACCCTGAAGTGTGAGTTTT	1620
Dp	1561	TCTCAGTGTCCCTCAAGTCTTGGAAATGTTTATCTAACCCTGAAGTGTGAGTTTT	1620
Qy	1621	CACCCATGGAAGCAATTAGTCTGACAGTACATGTTGATTCCTCTGATATATACAAAT	1680
Dp	1621	CACCCATGGAAGCAATTAGTCTGACAGTACATGTTGATTCCTCTGATATATACAAAT	1680
Qy	1681	ACATTTTTCCCTGTTATCTTGAACGTAACTTTTCCCTAAGAACACTTTTCTGCACCTTTC	1740
Dp	1681	ACATTTTTCCCTGTTATCTTGAACGTAACTTTTCCCTAAGAACACTTTTCTGCACCTTTC	1740
Qy	1741	ATTGTAAATAAAGAGTGTGCTGCACAACCTTAATCTTCTTTAATCTATGTTTCTTA	1800
Dp	1741	ATTGTAAATAAAGAGTGTGCTGCACAACCTTAATCTTCTTTAATCTATGTTTCTTA	1800
Qy	1801	CCTGATATATCAAAAAGAAATTCCTTATTTAATCTGTGACATATGTTCCCTGAGAA	1860
Dp	1801	CCTGATATATCAAAAAGAAATTCCTTATTTAATCTGTGACATATGTTCCCTGAGAA	1860
Qy	1861	TCATGTTCCCTTTATATGACTGAGGCAATTACTGACGTTGAGACTCAATCTTATATATAGT	1920

[illegible]

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RESULT 2
US-60-190-928-1
; Sequence 1, Application US/60190928
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR HAVING HOMOLOGY TO THE MAS PROTO-ONCOGENE, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING THIS HUMAN GPCR PROTEIN, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000387
; CURRENT APPLICATION NUMBER: US/60/190,928
; CURRENT FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: HUMAN
US-60-190-928-1

Query Match      100.0%; Score 2618; DB 84; Length 2618;

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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2618; Conservative 0;

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QY 1 AACAAATGCGGAAATTCGGGACGAGATGAATCTAGTTTAAAGGCTGAGACCT 60
Db 1 AACAAATGCGGAAATTCGGGACGAGATGAATCTAGTTTAAAGGCTGAGACCT 60
QY 61 CCTCCCTCTCTTACTCTCTCTCTCAACATGTGAGACGCTCCCTTTGCTTT 120
Db 61 CCTCCCTCTCTTACTCTCTCTCTCAACATGTGAGACGCTCCCTTTGCTTT 120
QY 121 CACCAAGATTGGAAGCTTCTGAGGCTTCCCAAGAGAGAGCTGCTATGCTTTGTA 180
Db 121 CACCAAGATTGGAAGCTTCTGAGGCTTCCCAAGAGAGAGCTGCTATGCTTTGTA 180
QY 181 CAGTCTGAGAGCTTTAGCCAGTTAAACCCATTTCTTATTAATTTCCAGTCTCAG 240
Db 181 CAGTCTGAGAGCTTTAGCCAGTTAAACCCATTTCTTATTAATTTCCAGTCTCAG 240
QY 241 TATTTCTTTTGAACAATTTGAGAAATGAATTAACAAGAGAGAGAGAGATGAA 300
Db 241 TATTTCTTTTGAACAATTTGAGAAATGAATTAACAAGAGAGAGAGAGATGAA 300
QY 301 ATCCCAAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 301 ATCCCAAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 361 TCCACGAGAAACGAGAAATTAAGAAATCCCACTGATGTGATACATAGAGGCACTCT 420
Db 361 TCCACGAGAAACGAGAAATTAAGAAATCCCACTGATGTGATACATAGAGGCACTCT 420
QY 421 TGGGATGTCAACAGAGATTAAGAAATGGAAGCAATCTCATGAGCTCATCAGCTG 480
Db 421 TGGGATGTCAACAGAGATTAAGAAATGGAAGCAATCTCATGAGCTCATCAGCTG 480
QY 481 GGTTCCTGAGATGGAATTCACCAATCCAGTCTTGGGTACAGAACTGAGACCAATCAAG 540
Db 481 GGTTCCTGAGATGGAATTCACCAATCCAGTCTTGGGTACAGAACTGAGACCAATCAAG 540
QY 541 GAGCTGAGAGAGACTCTTGTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 GAGCTGAGAGAGACTCTTGTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 TTTCCCTGTGCGGCTGACAGAGAAACGCGGTTGTGCTGTGCTCTGAGGCTGCGGATGC 660
Db 601 TTTCCCTGTGCGGCTGACAGAGAAACGCGGTTGTGCTGTGCTCTGAGGCTGCGGATGC 660
QY 661 GCAGAGAGAGCTGTCTCTCACTACATCTCACTGAGTGTGCGGAGAGAGAGAGAGAG 720
Db 661 GCAGAGAGAGCTGTCTCTCACTACATCTCACTGAGTGTGCGGAGAGAGAGAGAG 720
QY 721 GCGGACCAATATATATGTTGCGGTTACGCTCATCATATATATATATATATATATAT 780
Db 721 GCGGACCAATATATATGTTGCGGTTACGCTCATCATATATATATATATATATATAT 780
QY 781 TCTCTAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 TCTCTAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 GCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 ACCTGTCAATCGGATATGATGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 ACCTGTCAATCGGATATGATGCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 AGTGAATGTTCTGACTCTCTGTTAGTGTGCTGATTTCTTTGTTGTTGAAACGCTGAG 1020
Db 961 AGTGAATGTTCTGACTCTCTGTTAGTGTGCTGATTTCTTTGTTGTTGAAACGCTGAG 1020
QY 1021 ATTTCATTAACAATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 ATTTCATTAACAATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
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Db 1021 ATTTCATTAACAATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 TCTCTGCTGATGAGATTCCTGTGTGATCCCGAAGATCCGCTGATGATGATG 1140
Db 1081 TCTCTGCTGATGAGATTCCTGTGTGATCCCGAAGATCCGCTGATGATGATG 1140
QY 1141 CCATCTCTCTCAAGATGCTGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Db 1141 CCATCTCTCTCAAGATGCTGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1201 CCGTGTTCAGAGATCCAGCTGAGATGGAAGATCTTATTTGATATGATGATCTAGTT 1260
Db 1201 CCGTGTTCAGAGATCCAGCTGAGATGGAAGATCTTATTTGATATGATGATCTAGTT 1260
QY 1261 CCATTTTCTGCTGCTCTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 CCATTTTCTGCTGCTCTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 CCTTTAGGAGAGCTCAAAATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 CCTTTAGGAGAGCTCAAAATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 ACAAGCTGAGGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 ACAAGCTGAGGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 GAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 GAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
Db 1501 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1561 TCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Db 1561 TCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 CACCATGAGAGAGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 CACCATGAGAGAGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 ACATTTTCCCTGTTATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ACATTTTCCCTGTTATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 ATTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 ATTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 CCTGATAGATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 CCTGATAGATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 TCAATGCTGCTTTATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 TCAATGCTGCTTTATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1921 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
QY 1981 GAGAGAGATTCCTCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 1981 GAGAGAGATTCCTCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
QY 2041 CTGTATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
Db 2041 CTGTATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
QY 2101 GCGGCTTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2101 GCGGCTTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
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QY 2161 TGAGAGCCATATAATATGTCACCAAGTTTCATTTGGCCATTGGAACCTCAATATTTG 2220
DB 2161 TGAGAGCCATATAATATGTCACCAAGTTTCATTTGGCCATTGGAACCTCAATATTTG 2220
QY 2221 ATTTAAAGTGAATATATCTTGAACCAATTATATCTTACAGATTCCTTCAGTT 2280
DB 2221 ATTTAAAGTGAATATATCTTGAACCAATTATATCTTACAGATTCCTTCAGTT 2280
QY 2281 GTAGAGAAATCTTCAATCTTCCAGTTTGTATTAATTTGTTGATTTGATCTTCACT 2340
DB 2281 GTAGAGAAATCTTCAATCTTCCAGTTTGTATTAATTTGTTGATTTGATCTTCACT 2340
QY 2341 TAGTTTATGCTCTTTTACATGAGAGCAAACTGAAACCTGACCTTCCATGACAA 2400
DB 2341 TAGTTTATGCTCTTTTACATGAGAGCAAACTGAAACCTGACCTTCCATGACAA 2400
QY 2401 TCTCAATTAATGATCTGATATTAATCTTACAGTTGTACAGAAATTCGATACATGCTGT 2460
DB 2401 TCTCAATTAATGATCTGATATTAATCTTACAGTTGTACAGAAATTCGATACATGCTGT 2460
QY 2461 GACATACATGAACCTGGAATATTTGTCTAAGAGAAATTAAGCCGACGACCAATTTT 2520
DB 2461 GACATACATGAACCTGGAATATTTGTCTAAGAGAAATTAAGCCGACGACCAATTTT 2520
QY 2521 GTAGAGTCAATCTTATGAGGTATCCAAATTAGAGAAATTCCTTGAACACAGAAATTAATT 2580
DB 2521 GTAGAGTCAATCTTATGAGGTATCCAAATTAGAGAAATTCCTTGAACACAGAAATTAATT 2580
QY 2581 AGGAGATCTGTGTCTGAG 2618
DB 2581 AGGAGATCTGTGTGTGAG 2618

RESULT 3
US-60-190-928-1
; Sequence 1, Application US/60190928
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR HAVING HOMOLOGY TO THE MAS PROTO-ONCOGENE, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING THIS HUMAN GPCR PROTEIN, AND USES
; FILE REFERENCE: CL000387
; CURRENT APPLICATION NUMBER: US/60/190, 928
; CURRENT FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: HUMAN
US-60-190-928-1

Query Match 100.0%; Score 2618; DB 84; Length 2618;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACAAATGCGCGAATTCGACAGAGATGAATCTAGTTGTTTAAAGCGTGAACCT 60
DB 1 AACAAATGCGCGAATTCGACAGAGATGAATCTAGTTGTTTAAAGCGTGAACCT 60
QY 61 CTTCCCTCTCTCTTAACTCTGCTCTCAACATGTGAGAGCGCTCCCTCCCTTTGCTTT 120
DB 61 CTTCCCTCTCTCTTAACTCTGCTCTCAACATGTGAGAGCGCTCCCTCCCTTTGCTTT 120
QY 121 CACCAAGATTGGAAGCTTCTGAGGCTCCCGACAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 CACCAAGATTGGAAGCTTCTGAGGCTCCCGACAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 CAGTGTGTAGAGCTATTAGCGAGTTAAACCAATTCCTTCAATTAATTTCCAGTCTCAGG 240
DB 181 CAGTGTGTAGAGCTATTAGCGAGTTAAACCAATTCCTTCAATTAATTTCCAGTCTCAGG 240

QY 241 TATTTCTTTTATGCAATTTGAGATTAATGAACTATACAGACAGAGAGAGAGAGAGAGAGAG 300
DB 241 TATTTCTTTTATGCAATTTGAGATTAATGAACTATACAGACAGAGAGAGAGAGAGAGAGAG 300
QY 301 ATCCAGAGTGTCTTCTGCTGTCTTCAAGTCTCTGCTGTGTCTCTCCAGTGTCTCAAT 360
DB 301 ATCCAGAGTGTCTTCTGCTGTCTTCAAGTCTCTGCTGTGTCTCTCCAGTGTCTCAAT 360
QY 361 TCCACAGAAACCGAAATTAATAAGATTCACAGATGTGTATATATGAAAGCCACTCTCT 420
DB 361 TCCACAGAAACCGAAATTAATAAGATTCACAGATGTGTATATATGAAAGCCACTCTCT 420
QY 421 TGGAGTCAAAACAGATTAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 TGGAGTCAAAACAGATTAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 GGTTCAGAGATGATTCACATCCAGTCTTGGGTACAGAACTGACACCAATCAACG 540
DB 481 GGTTCAGAGATGATTCACATCCAGTCTTGGGTACAGAACTGACACCAATCAACG 540
QY 541 GACGTAGAGAGATCTTGTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 GACGTAGAGAGATCTTGTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 TTTCCCTGTGTGCGCTGACAGAGAAACGCGGTGTGTCTCTGAGCTCTGAGGCTGCGCATGC 660
DB 601 TTTCCCTGTGTGCGCTGACAGAGAAACGCGGTGTGTGTCTCTGAGCTCTGAGGCTGCGCATGC 660
QY 661 GCAGAGAGCGTGTCTCCATCTACATCTCAACCTGTGTGCGGCGGAGCTTCTCTCTTA 720
DB 661 GCAGAGAGCGTGTCTCCATCTACATCTCAACCTGTGTGCGGCGGAGCTTCTCTCTTA 720
QY 721 GCGGCGCATTAATATGTTGCGCGTTAGAGCTCATCAATATCCGCAATCCCATCTCCAAA 780
DB 721 GCGGCGCATTAATATGTTGCGCGTTAGAGCTCATCAATATCCGCAATCCCATCTCCAAA 780
QY 781 TCTCAGTCCGTGTATGATACCTTCTCTTATAGGCTTATAGGCTTATAGGCTTATAGGCTTAT 840
DB 781 TCTCAGTCCGTGTATGATACCTTCTCTTATAGGCTTATAGGCTTATAGGCTTATAGGCTTAT 840
QY 841 GCACGAGCGGTGTCTTCAATCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GCACGAGCGGTGTCTTCAATCTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 ACTGTGATGTGTATGTGTCTGTCTGTGAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 960
DB 901 ACTGTGATGTGTATGTGTCTGTCTGTGAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 960
QY 961 AGTGAATGTCTGTGATCTCTCTGTTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 961 AGTGAATGTCTGTGATCTCTCTGTTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
QY 1021 ATTTCAATTAATGAGT 1080
DB 1021 ATTTCAATTAATGAGT 1080
QY 1081 TCTGT 1140
DB 1081 TCTGT 1140
QY 1141 CCATCTCTCTCAAGT 1200
DB 1141 CCATCTCTCTCAAGT 1200
QY 1201 CCGT 1260
DB 1201 CCGT 1260
QY 1261 CCATTTTCTGT 1320
DB 1261 CCATTTTCTGT 1320

QY 1321 CCTTAAAGGAGGCTGCAAAATAGGAGCAAGCTGAGTCTCCAGAGGCTGACAG 1380
DB 1321 CCTTAAAGGAGGCTGCAAAATAGGAGCAAGCTGAGTCTCCAGAGGCTGACAG 1380
QY 1381 ACAGGCTGAGTGAATGAAGTGGCTTCTCCAGAGAAACCCGAGGCTGCG 1440
DB 1381 ACAGGCTGAGTGAATGAAGTGGCTTCTCCAGAGAAACCCGAGGCTGCG 1440
QY 1441 GAAGCAGATGAGAGAGAGAGAAACCTGCGCTGCAAGAGAGCTTTGAGAGCA 1500
DB 1441 GAAGCAGATGAGAGAGAGAGAAACCTGCGCTGCAAGAGAGCTTTGAGAGCA 1500
QY 1501 TGCTGCGCTGCAACCTTGAACAATATATGCAATTTTCTAGCCTTCCAGAAATG 1560
DB 1501 TGCTGCGCTGCAACCTTGAACAATATATGCAATTTTCTAGCCTTCCAGAAATG 1560
QY 1561 TCTGAGTGGTCCCTCAAGGCTCTGCAATGATGTTATCTAAGCTGAGAGCTGAGTTT 1620
DB 1561 TCTGAGTGGTCCCTCAAGGCTCTGCAATGATGTTATCTAAGCTGAGAGCTGAGTTT 1620
QY 1621 CACCAGTGAAGAGAGATGAGTGAACAATGTTGAGATTCCTGATATTAACAAT 1680
DB 1621 CACCAGTGAAGAGAGATGAGTGAACAATGTTGAGATTCCTGATATTAACAAT 1680
QY 1681 ACATTTTCCCTGATATCTTGAACAATGTTTCTGAGAGAGCTTTTCTGAGCTTTC 1740
DB 1681 ACATTTTCCCTGATATCTTGAACAATGTTTCTGAGAGAGCTTTTCTGAGCTTTC 1740
QY 1741 ATTGTAATTAAGAGAGTGGCTGCAACAACCTTAACCTCTTATATGTTTCTTA 1800
DB 1741 ATTGTAATTAAGAGAGTGGCTGCAACAACCTTAACCTCTTATATGTTTCTTA 1800
QY 1801 CCTGATAGTATCAAAAAGAGAGATTCCTTATATCTGCAAGATATGTTCCCTGAAAA 1860
DB 1801 CCTGATAGTATCAAAAAGAGAGATTCCTTATATCTGCAAGATATGTTCCCTGAAAA 1860
QY 1861 TCAGTGTCCCTTTATGAGTGAAGGATTAAGCTGAGTGAAGGCTTAATTAAGT 1920
DB 1861 TCAGTGTCCCTTTATGAGTGAAGGATTAAGCTGAGTGAAGGCTTAATTAAGT 1920
QY 1921 GAGTTCGCTACCTTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTA 1980
DB 1921 GAGTTCGCTACCTTAATTCATTAATTCATTAATTCATTAATTCATTAATTCATTA 1980
QY 1981 GAGAGAGATTCCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
DB 1981 GAGAGAGATTCCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
QY 2041 CTGTCATTTGTCACAGAGTGTGACATGTTGGCTTGTGTTTGAATTAAGACATGCTG 2100
DB 2041 CTGTCATTTGTCACAGAGTGTGACATGTTGGCTTGTGTTTGAATTAAGACATGCTG 2100
QY 2101 GCGCCCTCCCTGAGAGCTGGTAAAGTTTATTAATTAATTAATTAATTAATTAATTA 2160
DB 2101 GCGCCCTCCCTGAGAGCTGGTAAAGTTTATTAATTAATTAATTAATTAATTAATTA 2160
QY 2161 TGAGAGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2220
DB 2161 TGAGAGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2220
QY 2221 ATTTTAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2280
DB 2221 ATTTTAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2280
QY 2281 GTAGAGAGATTCCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2340
DB 2281 GTAGAGAGATTCCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2340
QY 2341 TAGTTTATGCTGTTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
DB 2341 TAGTTTATGCTGTTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY 2401 TCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2460

DB 2401 TCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2460
QY 2461 GACATACATGAG 2520
DB 2461 GACATACATGAG 2520
QY 2521 GTAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2580
DB 2521 GTAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2580
QY 2581 AGAGAGATTCCTGAG 2618
DB 2581 AGAGAGATTCCTGAG 2618

RESULT 4
US-09-721-588-4370
Sequence 4370, Application US/09721588
GENERAL INFORMATION:
APPLICANT: Geating, David P.
APPLICANT: Holzman, Douglas A.
APPLICANT: Villereal, Jean-Luc
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.2046-001
CURRENT APPLICATION NUMBER: US/09/721.588
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/167,381
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4370
LENGTH: 1453
TYPE: DNA
ORGANISM: Homo sapiens
US-09-721-588-4370

Query Match 49.6%; Score 1298; DB 32; Length 1453;
Best Local Similarity 100.0%; Pred. No. 6.7e-271;
Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GGGTCATGAGATCGGGGTTTCTGAGCATGATTAACCATCCCACTTTGGGTACAGAAC 525
DB 156 GGGTCATGAGATCGGGGTTTCTGAGCATGATTAACCATCCCACTTTGGGTACAGAAC 215
QY 526 TGACACCAATCAAGGAG 585
DB 216 TGACACCAATCAAGGAG 275
QY 586 GGGTCATGAGATCGGGGTTTCTGAGCATGATTAACCATCCCACTTTGGGTACAGAAC 645
DB 276 GGGTCATGAGATCGGGGTTTCTGAGCATGATTAACCATCCCACTTTGGGTACAGAAC 335
QY 646 TGGGCTGCGCATGAG 705
DB 336 TGGGCTGCGCATGAG 395
QY 706 ACTTCCTCTTCTTAG 765
DB 396 ACTTCCTCTTCTTAG 455
QY 766 ATCCCATCTCCAAAATCCCTGAGTCTGATGATGATGATGATGATGATGATGATGAT 825
DB 456 ATCCCATCTCCAAAATCCCTGAGTCTGATGATGATGATGATGATGATGATGATGATGAT 515
QY 826 TGTGAGGCGCATGAG 885
DB 516 TGTGAGGCGCATGAG 575
QY 886 GCGGCGGCGCGAGATACCTGATCGATGATGATGATGATGATGATGATGATGATGATG 945
DB 576 GCGGCGGCGCGAGATACCTGATCGATGATGATGATGATGATGATGATGATGATGATG 635

Qy	946	IGCGGAGATCTGAGAGGAGNAGTTCTGGACTTCCTGTTTAGAGGAGTCAATCTGTTT	1009
Db	636	TGCGGAGTACTGAGAGTGAGATGTTCTGTGACTTCTGTTTAGAGTGTCTAATCTGTTT	695
Qy	1006	GGTGTGAACGTCAAGATTTCAATTACATTCGCGTGCCTGTTTTTTTATATGTGTGCTCT	1065
Db	696	GGTGTGAACGTCAAGATTTCAATTACAAATCGGTGCCTGTTTTTTTATATGTGTGCTCT	755
Qy	1066	GTGGGTCAAGCTGATCTCTGCTGTGTCAGAGATTTCTCTGTGAGATCCCGAAGATGCCGCTGA	1125
Db	756	GTGGGTCAAGCTGATCTCTGCTGTGTCAGAGATTTCTCTGTGAGATCCCGAAGATGCCGCTGA	815
Qy	1126	CCAGGCTGTACGTGACCAATCCCTCCACAGTGTGATCTTCTCTCTCTGTGAGCTGCCCT	1185
Db	816	CCAGGCTGTACGTGACCAATCTCTCCACAGTGTGATCTTCTCTCTCTGTGAGCTGCCCT	875
Qy	1186	TTGGCATTCAAGTGGGCGCTGTGTTTTCAAGATTCACCTGATTTGAAAGTCTTATTTGTCTC	1245
Db	876	TTGGCATTCAAGTGGGCGCTGTGTTTTCAAGATTCACCTGATTTGAAAGTCTTATTTGTCTC	935
Qy	1246	ATGTGCATCTAGTTTCCATTTTCCGTGCGCTCTTAACAGAGTGCACCCCAATCATT	1305
Db	936	ATGTGCATCTAGTTTCCATTTTCCGTGCGCTCTTAACAGAGTGCACCCCAATCATT	995
Qy	1306	ACTTCTTGCTGGGCTCCTTTAGAGCAGCTCAAAATAGCAGAACCTGAAGCTGTCTCC	1365
Db	996	ACTTCTTGCTGGGCTCCTTTAGAGCAGCTCAAAATAGCAGAACCTGAAGCTGTCTCC	1055
Qy	1366	AGAGGAGCTTCTCAAGACAACGCTGAGTGAATGAAGTGAAGGTGCTTCTCAAGAAA	1425
Db	1056	AGAGGAGCTTCTCAAGACAACGCTGAGTGAATGAAGTGAAGGTGCTTCTCAAGAAA	1115
Qy	1426	CCCTGAGAGCTGTCCGGAAGACAGATTGAGAGCATGAGGAAGAACTGTGCCCTGTCAAGCA	1485
Db	1116	CCCTGAGAGCTGTCCGGAAGACAGATTGAGAGCATGAGGAAGAACTGTGCCCTGTCAAGCA	1175
Qy	1486	GGACTTTGAGAGCAATGTGCGCTGTGCCACCCCTTGACATTTATATGCAATTTTCTTAAGCT	1545
Db	1176	GGACTTTGAGAGCAATGTGCGCTGTGCCACCCCTTGACATTTATATGCAATTTTCTTAAGCT	1235
Qy	1546	TCTGCGCTCAAGAAATGTCTCAGTGTGCTTCAAGGCTTTCGAATAGATGTTATCTAACCT	1605
Db	1236	TCTGCGCTCAAGAAATGTCTCAGTGTGCTTCAAGGCTTTCGAATAGATGTTATCTAACCT	1295
Qy	1606	GACAGTTGCAATTTTCACCCAATGGAAGACATTTAGTCTGACAGTACCAATGTTTGATCTC	1665
Db	1296	GACAGTTGCAATTTTCACCCAATGGAAGACATTTAGTCTGACAGTACCAATGTTTGATCTC	1355
Qy	1666	CTTGATATTACCAATACATTTTCCCTGTATCTTGACCTGAATCTTTCCTACTGAACCT	1725
Db	1356	CTTGATATTACCAATACATTTTCCCTGTATCTTGACCTGAATCTTTCCTACTGAACCT	1415
Qy	1726	TTTTCTGCACTTTTCATGTGAATATAAAGATGTGCTT	1763
Db	1416	TTTTCTGCACTTTTCATGTGAATATAAAGATGTGCTT	1453

```

RESULT 5
US-09-634-754-740
: Sequence 740, Application US/09634754
: GENERAL INFORMATION:
: APPLICANT: Lal, Preeti
: APPLICANT: Au-Young, Janice
: APPLICANT: Guegler, Karl J.
: APPLICANT: Baughn, Mariah R.
: APPLICANT: Shah, Purni
: TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
: FILE REFERENCE: PA-0017 US
: CURRENT APPLICATION NUMBER: US/09/634,754
: CURRENT FILING DATE: 2000-08-07
: NUMBER OF SEQ ID NOS: 809
: SOFTWARE: PERL Program

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; SEQ ID NO 740
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: unsure
; LOCATION: 287, 299, 301, 305, 325, 329-330, 350-351, 361, 366, 371, 377
; NAME/KEY: unsure
; LOCATION: 395, 399, 407
; OTHER INFORMATION: a or g or c or t, unknown, or other
; NAME/KEY: misc.feature
; OTHER INFORMATION: incyte ID No: 1909132CT1
; PUBLICATION INFORMATION:
;
US-09-634-754-740

```

Query March	43.8%;	Score 1147;	DB 27;	Length 1557;
Best Local Similarity	100.0%;	Prod. No. 2.5e-238;		
Matches 1147;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
OY	766	ATCCATCTCCAAATCCTCAGTCCCTGANGACCTTTCCTACTTATATAGCCCTAAGCA	825	
Db	411	ATCCATCTCCAAATCCTCAGTCCCTGANGACCTTTCCTACTTATATAGCCCTAAGCA	470	
OY	826	TGCTGAGGCGCATGAGCACCGAGCGCTGCTGTCTGCATCTGTGGCCCATCTGTGTACCACT	885	
Db	471	TGCTGAGGCGCATGAGCACCGAGCGCTGCTGTCTGCATCTGTGGCCCATCTGTGTACCACT	530	
OY	886	GGCGCGCGCCGAGATACCTGTCAATCCGATGATGTGTGTCTGTGGCCCGTGTCCCGC	945	
Db	531	GGCGCGCGCCGAGATACCTGTCAATCCGATGATGTGTGTCTGTGGCCCGTGTCCCGC	590	
OY	946	TGCGAGATCTCGAGTGAATGTCTGTGACTTCTGTATGTAGTGTCGTGATCTGT	1005	
Db	591	TGCGAGATCTCGAGTGAATGTCTGTGACTTCTGTATGTAGTGTCGTGATCTGT	650	
OY	1006	GGTGTGAACGTCAAGATTCTATAAATCCGCTGGCTGTGTTTTTATGTGTGTTCT	1065	
Db	651	GGTGTGAACGTCAAGATTCTATAAATCCGCTGGCTGTGTTTTTATGTGTGTTCT	710	
OY	1066	GTGGGTCCAGCTGAGTCTGTCTGTGTCAAGATTCCTGTGAGATCCCGGAATGTCCGCTGA	1125	
Db	711	GTGGGTCCAGCTGAGTCTGTCTGTGTCAAGATTCCTGTGAGATCCCGGAATGTCCGCTGA	770	
OY	1126	CCAGGCTGTACGTGACCATCTCTCTCAAGTGTGTGTTCTCTCTGTGGCCCTG	1185	
Db	771	CCAGGCTGTACGTGACCATCTCTCTCAAGTGTGTGTTCTCTCTGTGGCCCTG	830	
OY	1186	TTGGCATTCAGTGGGCCCTGTTTTTCAGAGATCCACTGTGATGGAAAGTCTTATTTGTC	1245	
Db	831	TTGGCATTCAGTGGGCCCTGTTTTTCAGAGATCCACTGTGATGGAAAGTCTTATTTGTC	890	
OY	1246	ATGTGCAATCAAGTTTCCATTTTCCGTGCCGTCTTACAGAGTGGCAACCCCATCATTT	1305	
Db	891	ATGTGCAATCAAGTTTCCATTTTCCGTGCCGTCTTACAGAGTGGCAACCCCATCATTT	950	
OY	1306	ACTTCTTCGTGGGCTCTTTAGGCGAGGCTCAAAATAGGCAAGACCTGAGCTGTCTCC	1365	
Db	951	ACTTCTTCGTGGGCTCTTTAGGCGAGGCTCAAAATAGGCAAGACCTGAGCTGTCTCC	1010	
OY	1366	AGAGGGCTCTGCAAGACACGCTGAGGTGATGAAGTGAAGGCTGTCTCTCAAGAAA	1425	
Db	1011	AGAGGGCTCTGCAAGACACGCTGAGGTGATGAAGTGAAGGCTGTCTCTCAAGAAA	1070	
OY	1426	CCCTGAGAGCTGTGGGGAAGACATTTGAGAGATGAGAAAGAACTCTGCGCCCTGCAGCA	1485	
Db	1071	CCCTGAGAGCTGTGGGGAAGACATTTGAGAGATGAGAAAGAACTCTGCGCCCTGCAGCA	1130	
OY	1486	GGACTTTGAGAGCATCTGCTCCCTGCCACCTTGTGACATTTATATGCAATTTTCTTAAGCT	1545	
Db	1131	GGACTTTGAGAGCATCTGCTCCCTGCCACCTTGTGACATTTATATGCAATTTTCTTAAGCT	1190	
OY	1546	TTGCTCTCAGAATGTCTCAGTGTCCCTCAAGTCTTCCATATGATGTTTATCTAACCT	1605	

Db 1191 TCTGCTCAGAAAGTCTCAGTGTGCTCCAGAGCTTCGAAATAGATGTTTATCTAACCT 1250
Qy 1606 GACAGTTGACAGTTTTCACCCATGAAAGCATTAAGTCTGACAGTACATGTTTGAATTC 1665
Db 1251 GACAGTTGACAGTTTTCACCCATGAAAGCATTAAGTCTGACAGTACATGTTTGAATTC 1310
Qy 1666 CTGATATTTACCAATACATTTTCCCTGTTATCTTGACAGTAACTCTTCTACTGAACCT 1725
Db 1311 CTGATATTTACCAATACATTTTCCCTGTTATCTTGACAGTAACTCTTCTACTGAACCT 1370
Qy 1726 TTTTCTGACATTTTCAATGTAATAAAGAGTTGCTGTCACAACTTAACTCTTCT 1785
Db 1371 TTTTCTGACATTTTCAATGTAATAAAGAGTTGCTGTCACAACTTAACTCTTCT 1430
Qy 1786 TATACCTGTTTCTTCACTGATAGTATCAAAAAGAGATTCCTTATTAATCTGTCAGACT 1845
Db 1431 TATACCTGTTTCTTCACTGATAGTATCAAAAAGAGATTCCTTATTAATCTGTCAGACT 1490
Qy 1846 ATGTTCCCTGAAATCAATGTTCCCTTTTATGACTGAGGCAATTAAGTGAAGCT 1905
Db 1491 ATGTTCCCTGAAATCAATGTTCCCTTTTATGACTGAGGCAATTAAGTGAAGCT 1550
Qy 1906 CAATTC 1912
Db 1551 CAATTC 1557

RESULT 6

US-09-634-754C-740

Sequence 740, Application US/09634754C
GENERAL INFORMATION:
APPLICANT: Lal, Preeti.
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Shah, Puri
TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
FILE REFERENCE: PA-0017 US
CURRENT APPLICATION NUMBER: US/09/634,754C
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 809
SOFTWARE: PERL Program
SEQ ID NO 740
LENGTH: 1557
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: unsure
LOCATION: 287, 299, 301, 305, 325, 329-330, 350-351, 361, 366, 371, 377
FEATURE:
NAME/KEY: unsure
LOCATION: 395, 399, 407
OTHER INFORMATION: a or g or c or t, unknown, or other
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inocyte ID No: 1909132CT1
PUBLICATION INFORMATION:
US-09-634-754C-740

Query Match 43.8%; Score 1147; DB 27; Length 1557;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 1147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 766 ATCCATCTCCAAATCCCTCAGTCCGTGATGACCTTTCCCTTATATAGGCTTAAGA 825
Db 411 ATCCATCTCCAAATCCCTCAGTCCGTGATGACCTTTCCCTTATATAGGCTTAAGA 470
Qy 826 TGCTAGGCGCATCAGACCGAGCGCTGCTGCTCACTCTGAGCCCATCTGTAACCT 885
Db 471 TGCTAGGCGCATCAGACCGAGCGCTGCTGCTCACTCTGAGCCCATCTGTAACCT 530
Qy 886 GCGCGCGCGCGCATACCTGTATGCTGTATGTGTCTGCTGTGGCGCTGTCCCTGC 945
Db 1551 GCGCGCGCGCGCATACCTGTATGCTGTATGTGTCTGCTGTGGCGCTGTCCCTGC 945

Db 531 GCGCGCGCGCGCATACCTGTATGCTGTATGTGTCTGCTGTGGCGCTGTCCCTGC 590
Qy 946 TCGAGATATCTGAGATGAGATGTTCTGTAATTCCTGTTAGTGTGCTGATTCCTGTT 1005
Db 591 TCGAGATATCTGAGATGAGATGTTCTGTAATTCCTGTTAGTGTGCTGATTCCTGTT 650
Qy 1006 GGTGTGAACCTGCAATTTCAATTAACATCGGTGTGCTGTTTATATGTGTGTTCTCT 1065
Db 651 GGTGTGAACCTGCAATTTCAATTAACATCGGTGTGCTGTTTATATGTGTGTTCTCT 710
Qy 1066 GTGGGTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125
Db 711 GTGGGTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Qy 1126 CAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1185
Db 771 CAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 830
Qy 1186 TTGGCATTCAGTGGGCTGTTTTCAGAGATTCACCTGATTTGGAAGTCTTATTTGTC 1245
Db 831 TTGGCATTCAGTGGGCTGTTTTCAGAGATTCACCTGATTTGGAAGTCTTATTTGTC 890
Qy 1246 ATGTGATCTAGTTTCAATTTTCTGTCGCTCTTAAAGAGTGCACACCCATCTT 1305
Db 891 ATGTGATCTAGTTTCAATTTTCTGTCGCTCTTAAAGAGTGCACACCCATCTT 950
Qy 1306 ACTTCTGTGAGGCTCTTATGAGCAGCTCAAAATAGCAGAACCTGAGCTGTTCTC 1365
Db 951 ACTTCTGTGAGGCTCTTATGAGCAGCTCAAAATAGCAGAACCTGAGCTGTTCTC 1010
Qy 1366 AAGAGGCTCTGAGACAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1425
Db 1011 AAGAGGCTCTGAGACAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1070
Qy 1426 CCTGAGCTGCTGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1485
Db 1071 CCTGAGCTGCTGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
Qy 1486 GAGCTTGTGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1545
Db 1131 GAGCTTGTGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1190
Qy 1546 TCTGCTCAGAAATGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1605
Db 1191 TCTGCTCAGAAATGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1250
Qy 1606 GACAGTTGATTTTCAACCATGAAAGCATTAAGTCTGACAGTACATGTTTGAATTC 1665
Db 1251 GACAGTTGATTTTCAACCATGAAAGCATTAAGTCTGACAGTACATGTTTGAATTC 1310
Qy 1666 CTGATATTTACCAATACATTTTCCCTGTTATCTTGACAGTAACTCTTCTACTGAACCT 1725
Db 1311 CTGATATTTACCAATACATTTTCCCTGTTATCTTGACAGTAACTCTTCTACTGAACCT 1370
Qy 1726 TTTTCTGACATTTTCAATGTAATAAAGAGTTGCTGTCACAACTTAACTCTTCT 1785
Db 1371 TTTTCTGACATTTTCAATGTAATAAAGAGTTGCTGTCACAACTTAACTCTTCT 1430
Qy 1786 TATACCTGTTTCTTCACTGATAGTATCAAAAAGAGATTCCTTATTAATCTGTCAGACT 1845
Db 1431 TATACCTGTTTCTTCACTGATAGTATCAAAAAGAGATTCCTTATTAATCTGTCAGACT 1490
Qy 1846 ATGTTCCCTGAAATCAATGTTCCCTTTTATGACTGAGGCAATTAAGTGAAGCT 1905
Db 1491 ATGTTCCCTGAAATCAATGTTCCCTTTTATGACTGAGGCAATTAAGTGAAGCT 1550
Qy 1906 CAATTC 1912
Db 1551 CAATTC 1557

RESULT 7

US-09-634-754D-740

Query Match 43.8%; Score 1147; DB 61; Length 1557;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 1147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 766 ATCCATTCCTCAAAATCTCTCACTCTGTATATGACCTTTTCCCACTTTAATAGGCTTAAGA 825
DB 411 ATCCATTCCTCAAAATCTCTCACTCTGTATATGACCTTTTCCCACTTTAATAGGCTTAAGA 470
QY 826 TGTGAGGCGCATCAGACACCGAGCGCTGCTGCATCTGTAGGCGCATCTGTACACT 885
DB 471 TGTGAGGCGCATCAGACACCGAGCGCTGCTGCATCTGTAGGCGCATCTGTACACT 530
QY 886 GCGCGCGCGCGCATATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGT 945
DB 531 GCGCGCGCGCGCATATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGT 590
QY 946 TGGCGAGATCTGTAGAGTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGT 1005
DB 591 TGGCGAGATCTGTAGAGTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGT 650
QY 1006 GGTGTGAACGTCAGATTTCAATATGCGTGTGTATTTTATATGTATGTATGTATGTATGTAT 1065
DB 651 GGTGTGAACGTCAGATTTCAATATGCGTGTGTATTTTATATGTATGTATGTATGTATGTAT 710
QY 1066 GTGGGTCCAGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1125
DB 711 GTGGGTCCAGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 770
QY 1126 CCAGGCTGTATGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1185
DB 771 CCAGGCTGTATGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 830
QY 1186 TTGGCATTCAGTGGGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1245
DB 831 TTGGCATTCAGTGGGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 890
QY 1246 ATGTGATCTATGTTTCAATTTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1305
DB 891 ATGTGATCTATGTTTCAATTTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 950
QY 1306 ACTTCTGTGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1365
DB 951 ACTTCTGTGTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1010
QY 1366 AGAGGGCTCTGAGGACACGCTGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTAT 1425
DB 1011 AGAGGGCTCTGAGGACACGCTGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTAT 1070
QY 1426 CCTGTGAGCTGTGCGGAAAGCAATTTGAGCACTGTGAGGAAACCTGTGCTGTGTGTGTGT 1485
DB 1071 CCTGTGAGCTGTGCGGAAAGCAATTTGAGCACTGTGAGGAAACCTGTGCTGTGTGTGTGT 1130
QY 1486 GGACTTTGAGGCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1545
DB 1131 GGACTTTGAGGCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1190
QY 1546 TCTGCTCAGAAATGTCTCAGTGTCTCTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAG 1605
DB 1191 TCTGCTCAGAAATGTCTCAGTGTCTCTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAG 1250
QY 1606 GACAGTTGAGTTTCAACCATGAAAGCAATTTGAGCACTGTGAGGAAACCTGTGCTGTGTGT 1665
DB 1251 GACAGTTGAGTTTCAACCATGAAAGCAATTTGAGCACTGTGAGGAAACCTGTGCTGTGTGT 1310
QY 1666 CTGTATATTAACAATATTTTCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTAT 1725
DB 1311 CTGTATATTAACAATATTTTCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTAT 1370
QY 1726 TTTTCTGACATTTTCAATTTGATATTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1785
DB 1371 TTTTCTGACATTTTCAATTTGATATTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1430
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QY 1786 TATACCTGTTCTCTACCTGATAGTATCAAAAGAAATTTCTTATTTATCTGTACACT 1845
DB 1431 TATACCTGTTCTCTACCTGATAGTATCAAAAGAAATTTCTTATTTATCTGTACACT 1490
QY 1846 ATGTCCCGCGTGAATATGTTCCCTTTATGACTGTGAGGCAATCTGACATTTGGAAGCT 1905
DB 1491 ATGTCCCGCGTGAATATGTTCCCTTTATGACTGTGAGGCAATCTGACATTTGGAAGCT 1550
QY 1906 CAATCT 1912
DB 1551 CAATCT 1557
```

RESULT 9

US-09-532-367-55
Sequence 55, Application US/09532367

GENERAL INFORMATION:

```
APPLICANT: Hodgson, David M.
APPLICANT: Lincoln, Stephen E.
APPLICANT: Russo, Frank D.
APPLICANT: Spiro, Peter A.
APPLICANT: Banville, Steve C.
APPLICANT: Bratcher, Shawn R.
APPLICANT: Dufour, Gerard E.
APPLICANT: Cohen, Howard J.
APPLICANT: Rosen, Bruce
APPLICANT: Chalup, Michael S.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Jones, Antisea L.
APPLICANT: Yu, Jimmy Y.
APPLICANT: Greenawalt, Lila B.
APPLICANT: Panzer, Scott R.
APPLICANT: Roseberry, Ann M.
APPLICANT: Wright, Rachel J.
TITLE OF INVENTION: RECEPTOR MOLECULES
FILE REFERENCE: PT-0005 US
CURRENT APPLICATION NUMBER: US/09/532,367
CURRENT FILING DATE: 2000-03-21
EARLIER APPLICATION NUMBER: 60/125,366; 60/126,218; 60/126,247; 60/126,590; 60/125,792
EARLIER FILING DATE: 1999-03-19; 1999-03-25; 1999-03-24; 1999-03-26; 1999-03-23;
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PERL Program
SEQ ID NO 55
LENGTH: 1146
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 338589.1
US-09-532-367-55
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Query Match 43.8%; Score 1146; DB 23; Length 1146;
Best Local Similarity 100.0%; Pred. No. 4.5e-238;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 762 GCGCATCCCATCTCAAAATCTCTCACTCTGTATATGACCTTTTCCCACTTTAATAGGCTTA 821
DB 1 GCGCATCCCATCTCAAAATCTCTCACTCTGTATATGACCTTTTCCCACTTTAATAGGCTTA 60
QY 822 AGCATGAGGCGCATCAGACACGAGCGCTGCTGCATCTGTGAGGCGCATCTGTGAGGCGCAT 881
DB 61 AGCATGAGGCGCATCAGACACGAGCGCTGCTGCATCTGTGAGGCGCATCTGTGAGGCGCAT 120
QY 882 CACTGCGCGCGCGCATATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGT 941
DB 121 CACTGCGCGCGCGCATATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGT 180
QY 942 CTGTGCGGAGTATCTGTAGAGTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCT 1001
DB 181 CTGTGCGGAGTATCTGTAGAGTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCT 240
QY 1002 GTTTGTGGAACGTCAGATTTCAATATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1061
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Db	241	GTTTGGGTGAAAAGCTGAGATTTCATTAACAATCGGTGGCTGGTTTTTTTATATGATGGATT	300
Qy	1062	CTCTGTGGGCTCAACCTGTGTCTGTGTGTGAGATTCTCTGTGATCCCGAAGATGCGG	1121
Db	301	CTCTGTGGGCTCAACCTGTGTCTGTGTGTGAGATTCTCTGTGATCCCGAAGATGCGG	360
Qy	1122	CTGACCAAGGCGTATACGTGACATCTCTCTCAAGTGCAGGTCCTTCTCTGTGGACCTG	1181
Db	361	CTGACCAAGGCGTATACGTGACATCTCTCTCAAGTGCAGGTCCTTCTCTGTGGACCTG	420
Qy	1182	CCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGATCCACCTGATATGGAAAGTCATATT	1241
Db	421	CCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGATCCACCTGATATGGAAAGTCATATT	480
Qy	1242	TGTGATGTGACATCTAGATTCCATTTTCTGTCCGCTCTTAAACAGAGTGCACCCATC	1301
Db	481	TGTGATGTGACATCTAGATTCCATTTTCTGTCCGCTCTTAAACAGAGTGCACCCATC	540
Qy	1302	ATTTACTTCTGTGGGGCTCCTTTAAGGAGGCTCAAAATPAGGCAACCTGACGTGATT	1361
Db	541	ATTTACTTCTGTGGGGCTCCTTTAAGGAGGCTCAAAATPAGGCAACCTGACGTGATT	600
Qy	1362	CTCCAGAGGGCTCTGACGAGACACGCTGAGGTGATGAAAGGTGAGGGTGTGCTTCTAG	1421
Db	601	CTCCAGAGGGCTCTGACGAGACACGCTGAGGTGATGAAAGGTGAGGGTGTGCTTCTAG	660
Qy	1422	GAAAACCTTGAGCTGTGCGGAAGCAGATTGAGCAGTGAAGAGAACCTTGTCCCTGTCA	1481
Db	661	GAAAACCTTGAGCTGTGCGGAAGCAGATTGAGCAGTGAAGAGAACCTTGTCCCTGTCA	720
Qy	1482	GACAGGACTTTGAGAGCAATGCTGCCCTGCCACCTTGACAATTAATGCAATTTTCTTA	1541
Db	721	GACAGGACTTTGAGAGCAATGCTGCCCTGCCACCTTGACAATTAATGCAATTTTCTTA	780
Qy	1542	GCCTTTCGCCCTCAGAAATGTCACAGTGTGCCCTCAAGGCTTTCGAAATGATGTTATCTA	1601
Db	781	GCCTTTCGCCCTCAGAAATGTCACAGTGTGCCCTCAAGGCTTTCGAAATGATGTTATCTA	840
Qy	1602	ACCTGACAGTTGACAGTTTCAACCCATGGAAGCATTTAGCTGACAGTACCAATGTTGGAT	1661
Db	841	ACCTGACAGTTGACAGTTTCAACCCATGGAAGCATTTAGCTGACAGTACCAATGTTGGAT	900
Qy	1662	TCTCCTTGATATTACCAATACATTTCCCTGTATCTTGCACTGAATCTTTCCTACTGAA	1721
Db	901	TCTCCTTGATATTACCAATACATTTCCCTGTATCTTGCACTGAATCTTTCCTACTGAA	960
Qy	1722	CACATTTTCTGACATTTTCATTTGTAATAAAGAGTGTCTGTCCACCAACCTTAACACTCT	1781
Db	961	CACATTTTCTGACATTTTCATTTGTAATAAAGAGTGTGTGTCCACCAACCTTAACACTCT	1020
Qy	1782	TCTTTATATCTGTTCTTCACTGTGATGATCAAAAAGAGATTCCTTATTTATCTGTCA	1841
Db	1021	TCTTTATATCTGTTCTTCACTGTGATGATCAAAAAGAGATTCCTTATTTATCTGTCA	1080
Qy	1842	GACTATGTTCCCTGGAATAATCATGTTCCCTTTATGACTGAGGCAATTAATGCAAGTTGGA	1901
Db	1081	GACTATGTTCCCTGGAATAATCATGTTCCCTTTATGACTGAGGCAATTAATGCAAGTTGGA	1140
Qy	1902	AGCTCA 1907	
Db	1141	AGCTCA 1146	

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RESULT 10
US-09-867-570-3
; Sequence 3, Application US/09867570
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CU000900-CIP
; CURRENT APPLICATION NUMBER: US/09/867,570

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: CURRENT FILING DATE: 2001-05-31
: PRIOR APPLICATION NUMBER: 09/695,045
: PRIOR FILING DATE: 2000-10-25
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0.
: SEQ ID NO 3
: LENGTH: 8622
: TYPE: DNA
: ORGANISM: Human
US-09-867-570-3

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Query Match	42.1%;	Score 1101;	DB 36;	Length 8622;
Best Local Similarity	100.0%;	Pred. No. 1.3e-228;		
Matches 1101;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.

OY	466	GGGATCATCAGCTGGGGGTTTCTGAGCAATGAAATTCAAACATCCAGCTTGGGATCAGAAAC	525
Dd	7502	GGGATCATCAGCTGGGGGTTTCTGAGCATGAAATTCAAACATCCAGCTTGGGATCAGAAAC	7566
OY	526	TGACACCAATCAACGAGAGTGAGGAGACTCCTTGCTACAGACAGACCTTGAGCTTACAGG	585
Dd	7562	TGACACCAATCAACGAGAGTGAGGAGACTCCTTGCTACAGACAGACCTTGAGCTTACAGG	7622
OY	586	GGCTGACGTGATGTTTCCCTTGTGCGGCTGACAGGAAAGCGGGTTGTGCTTGGGCTCC	645
Dd	7622	GGCTGACGTGATGTTTCCCTTGTGCGGCTGACAGGAAAGCGGGTTGTGCTTGGGCTCC	7682
OY	646	TGGGCTGCGCGATGCGAGAAACGTGCTCCATCTACATCCTCAACCTGGTCGGGCGG	705
Dd	7682	TGGGCTGCGCGATGCGAGAAACGTGCTCCATCTACATCCTCAACCTGGTCGGGCGG	7742
OY	706	ACTTCCTCTTCTTAGCGGCGACATTAATATGTTGGCGGTTACGCTCATCAATATCCGCC	765
Dd	7742	ACTTCCTCTTCTTAGCGGCGACATTAATATGTTGGCGGTTACGCTCATCAATATCCGCC	7802
OY	766	ATCCCATCTCCAAAATCCTCAGTCTCTGATGACCTTTCCCTACTTTATAGGCTTAAACA	825
Dd	7802	ATCCCATCTCCAAAATCCTCAGTCTCTGATGACCTTTCCCTACTTTATAGGCTTAAACA	7862
OY	826	TGCTGAGGCGCATCAGACACGAGCGCTGCTCCATCTCTGCGCCACTTGCTGACACT	885
Dd	7862	TGCTGAGGCGCATCAGACACGAGCGCTGCTCCATCTCTGCGCCACTTGCTGACACT	7922
OY	886	GC CGCGCGCCAGATACCTGTCAATCGATGATGTGTCTGCTCTGGGCCCTGTCCCTGC	945
Dd	7922	GC CGCGCGCCAGATACCTGTCAATCGATGATGTGTCTGCTCTGGGCCCTGTCCCTGC	7982
OY	946	TGCGGAGTATCCTGAGAGTGAATGTTTCTGTACTTCTCGTTTAGAGAGCTGATTTCTGTT	1002
Dd	7982	TGCGGAGTATCCTGAGAGTGAATGTTTCTGTACTTCTCGTTTAGAGAGCTGATTTCTGTT	8042
OY	1006	GGTGTGAAAACGTCAAGATTTCAATCAATCGAGTGAGCTGGTTTTTTTATGTGATGTTCTCT	1065
Dd	8042	GGTGTGAAAACGTCAAGATTTCAATCAATCGAGTGAGCTGGTTTTTTTATGTGATGTTCTCT	8102
OY	1066	GTGGGTCACGCTGGTCTGCTGTGAGAGATTTCTGTGATCCCGAAGATGCCGCTGA	1122
Dd	8102	GTGGGTCACGCTGGTCTGCTGTGAGAGATTTCTGTGATCCCGAAGATGCCGCTGA	8162
OY	1126	CCAGGCTGTAGTGAACCATCTCTCTCAAGAGTGTGTTCTCTCCTGTGGGCGTGGCCT	1188
Dd	8162	CCAGGCTGTAGTGAACCATCTCTCTCAAGAGTGTGTTCTCTCCTGTGGGCGTGGCCT	8222
OY	1186	TTGGCATTCAGTGGGCGCTGTGTTTTCAAGATTCACCTGATTTGAAAATCTTAATTTGTC	1245
Dd	8222	TTGGCATTCAGTGGGCGCTGTGTTTTCAAGATTCACCTGATTTGAAAATCTTAATTTGTC	8282
OY	1246	ATGTGCAATCAGTTTCCATTTTCTGTCCGCTTTTACAGACAGTGCACACCCCATCATTT	1302
Dd	8282	ATGTGCAATCAGTTTCCATTTTCTGTCCGCTTTTACAGACAGTGCACACCCCATCATTT	8342
OY	1306	ACTTCTTCGTGGGCTCCTTTAGGACAGGCTCAAAATAGCAGAACTGTAGAGCTGTTCTCC	1366

NAME/KEY: CDS
LOCATION: (201) ... (1169)
US-10-292-798-1273

Query Match 41.7%; Score 1093; DB 50; Length 1369;
Best Local Similarity 99.8%; Pred. No. 1.2e-226;
Matches 1193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

466 GGGGTCATCAGACGCGGGTTCTGAGCATGATTCACATCCAGCTGTTGGGTACAGAAC 525
175 GGGTCATCAGACGCGGGTTCTGAGCATGATTCACATCCAGCTGTTGGGTACAGAAC 234
526 TGACACCAATCAACGAGCGTGAAGAGACTCTTCTCAAGACAGACCTGAGCTTCAAG 585
235 TGACACCAATCAACGAGCGTGAAGAGACTCTTCTCAAGACAGACCTGAGCTTCAAG 294
586 GGGTCATCAGACGCGGGTTCTGAGCATGATTCACATCCAGCTGTTGGGTACAGAAC 645
295 GGGTCATCAGACGCGGGTTCTGAGCATGATTCACATCCAGCTGTTGGGTACAGAAC 354
646 TGGGTCGCGGCGACGAGAGAGCGTCTCCATCTCAATCCATCCATCCATCCATCC 705
355 TGGGTCGCGGCGACGAGAGAGCGTCTCCATCTCAATCCATCCATCCATCCATCC 414
706 ACTTCTCTCTCTTACGCGGACATTAATATGTCGCGGTTACGCGGTTACATTAAT 765
415 ACTTCTCTCTCTTACGCGGACATTAATATGTCGCGGTTACGCGGTTACATTAAT 474
766 ATCCCATCTCCAAATCTCAAGTCTGTGATGACCTTCCCTTATATAGGCTTAAGCA 825
475 ATCCCATCTCCAAATCTCAAGTCTGTGATGACCTTCCCTTATATAGGCTTAAGCA 534
826 TGGTCGCGGCGACGAGAGAGCGTCTCCATCTCAATCCATCCATCCATCCATCC 885
535 TGGTCGCGGCGACGAGAGAGCGTCTCCATCTCAATCCATCCATCCATCCATCC 594
886 GCGCGCGCGGCGACGAGAGAGCGTCTCCATCTCAATCCATCCATCCATCCATCC 945
595 GCGCGCGCGGCGACGAGAGAGCGTCTCCATCTCAATCCATCCATCCATCCATCC 654
946 TGGGAGATCTGAGAGTGTCTGTGACCTTCTGTTAGTGTGATCTGTTT 1005
655 TGGGAGATCTGAGAGTGTCTGTGACCTTCTGTTAGTGTGATCTGTTT 714
1006 GGTGTGAAAGTCAAGATTTCAATCAATCCGCGGCTGTTTATATGTTGTTCT 1065
715 GGTGTGAAAGTCAAGATTTCAATCAATCCGCGGCTGTTTATATGTTGTTCT 774
1066 GTGGGTCACGCTGATCTGCTGAGTCAAGATTTCTGTGATCCGGAAGATGCGGCTGA 1125
775 GTGGGTCACGCTGATCTGCTGAGTCAAGATTTCTGTGATCCGGAAGATGCGGCTGA 834
1126 CCAAGGTCGATGACCATCTCTCAAGTGTGATCTTCTCTGTCGCTGCT 1185
835 CCAAGGTCGATGACCATCTCTCAAGTGTGATCTTCTCTGTCGCTGCT 894
1186 TTGGGTCATGAGTGGGCTGTTTTCAGATTCACCTGATGGAAGTCTTATTTGTC 1245
895 TTGGGTCATGAGTGGGCTGTTTTCAGATTCACCTGATGGAAGTCTTATTTGTC 954
1246 ATGTGATCTAGTTCATTTCTGTCGCTCTTAACAGAGGCAAGCCCATCATTT 1305
955 ATGTGATCTAGTTCATTTCTGTCGCTCTTAACAGAGGCAAGCCCATCATTT 1014
1306 ACTTCTCTGAGGCTCTTTAGGAGCGTCAAAATAGGAGAACTGAGTGTCTCC 1365
1015 ACTTCTCTGAGGCTCTTTAGGAGCGTCAAAATAGGAGAACTGAGTGTCTCC 1074
1366 AGAGGCTCTGAGAGACGCTGATGATGAAGTGAAGGTTGCTTCTCAAGAAA 1425
1075 AGAGGCTCTGAGAGACGCTGATGATGAAGTGAAGGTTGCTTCTCAAGAAA 1134
1426 CCTGAGAGTGTGGGAGGAGATTTGAGAGAGTGAAGAGAACTCTGCTGTCAACA 1485

1135 CCTGAGAGTGTGGGAGGAGATTTGAGAGAGTGAAGAGAACTCTGCTGTCAACA 1194
1486 GGAATTTGAGAGAAAGCTGCTGCGACCTTGAACATTAATATGATTTTCTAGCCT 1545
1195 GGAATTTGAGAGAAAGCTGCTGCGACCTTGAACATTAATATGATTTTCTAGCCT 1254
1546 TCGGCTCAGAAATGCTCAGTGTGCTGCTCAAGGTTTCGAATAGATTTTAACT 1605
1255 TCGGCTCAGAAATGCTCAGTGTGCTGCTCAAGGTTTCGAATAGATTTTAACT 1314
1606 GACAGTTGACGTTTCAACCATGAGAAAGATTAATGCTGACAGTCAATGTTTGA 1660
1315 GACAGTTGACGTTTCAACCATGAGAAAGATTAATGCTGACAGTCAATGTTTGA 1369

RESULT 13

PCT-US01-14519-30
Sequence 30, Application PCT/US0114519
GENERAL INFORMATION:
APPLICANT: California Institute of Technology
APPLICANT: Dong, Xinzhang
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-Kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE. 004VPC
CURRENT APPLICATION NUMBER: PCT/US01/14519
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US unknown
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (332) ... (1297)
PCT-US01-14519-30

Query Match 41.6%; Score 1088; DB 1; Length 1400;
Best Local Similarity 100.0%; Pred. No. 1.4e-225;
Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

473 CAGACTGGGTTTCTGAGCATGATTCACATCCAGCTTGGGTACAGAACTGACACC 532
313 CAGACTGGGTTTCTGAGCATGATTCACATCCAGCTTGGGTACAGAACTGACACC 372
533 AATCAACGAGCGTGAAGAGACTCTTGTCTAAGACAGACCTTGAAGCTTCAAGGCTGAC 592
373 AATCAACGAGCGTGAAGAGACTCTTGTCTAAGACAGACCTTGAAGCTTCAAGGCTGAC 432
593 GTGATCGTTTCTGTCGCGGCTGAAGAGAAAGGCTGTGCTGCGGCTGCGGCTG 652
433 GTGATCGTTTCTGTCGCGGCTGAAGAGAAAGGCTGTGCTGCGGCTGCGGCTG 492
653 CCGCATCGAGAGACGCTGCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCT 712
493 CCGCATCGAGAGACGCTGCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCT 552
713 CTTCCTTACGCGGCAATTAATATGTTGCGGTTACGCTCATCAATATCCGCAATCCAT 772
553 CTTCCTTACGCGGCAATTAATATGTTGCGGTTACGCTCATCAATATCCGCAATCCAT 612

Db 1153 CGTGGGCTCTTTAGGAGGCGTCAAAAATAGCAGAACCTTGAGCTGTCTCCAGAGGGC 1212
Qy 1373 TCTGACAGACACGCTGAGGTGATGAGGTGAGGGGCTTCTCAGAGAAACCTGGA 1432
Db 1213 TCTGACAGACACGCTGAGGTGATGAGGTGAGGGGCTTCTCAGAGAAACCTGGA 1272
Qy 1433 GCTGTGGGAGAGATTTGAGCAGTGAAGAAAGCTGTGCTCTGACAGAGACTTT 1492
Db 1273 GCTGTGGGAGAGATTTGAGCAGTGAAGAAAGCTGTGCTCTGACAGAGACTTT 1332
Qy 1493 GAGAGCAATGCTGCTGCTGCTGACCTTGAACAATTATATGATTTTCTTACCTTGTGCT 1552
Db 1333 GAGAGCAATGCTGCTGCTGCTGACCTTGAACAATTATATGATTTTCTTACCTTGTGCT 1392
Qy 1553 CAGAAATG 1560
Db 1393 CAGAAATG 1400

RESULT 15

US-09-849-869A-30

Sequence 30, Application US/09849869A

GENERAL INFORMATION:

APPLICANT: Anderson, David J.

APPLICANT: Dong, Xinzhong

APPLICANT: Zylka, Mark

APPLICANT: Simon, Melvin

APPLICANT: Han, Sang-kyou

TITLE OF INVENTION: PAIN SIGNALING MOLECULES

FILE REFERENCE: CALTE.004C1

CURRENT APPLICATION NUMBER: US/09/849, 869A

PRIOR APPLICATION NUMBER: 2001-05-04

PRIOR FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: US 60/202,027

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: US 09/704,707

PRIOR FILING DATE: 2000-11-03

PRIOR APPLICATION NUMBER: US 60/285,493

PRIOR FILING DATE: 2001-04-19

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 4.0.

SEQ ID NO 30

LENGTH: 1400

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (332)...(1297)

US-09-849-869A-30

Query Match 41.6%; Score 1088, DB 35; Length 1400;

Best Local Similarity 100.0%; Pred. No. 1,4e-225;

Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 473 CAGACTGGGGTTTCTGAGCATGATTAACCATCCGATCTGGGTACAGAACTGACACC 532
Db 313 CAGACTGGGGTTTCTGAGCATGATTAACCATCCGATCTGGGTACAGAACTGACACC 372
Qy 533 AATCAACGAGCGTGAAGAGACTCTTGTCTACAGACAGACCTTGAAGCTTCAAGGGGCTGAC 592
Db 373 AATCAACGAGCGTGAAGAGACTCTTGTCTACAGACAGACCTTGAAGCTTCAAGGGGCTGAC 432
Qy 593 GTGATGCTTTCTTCTGTGCGGCTGACAGAGAAAGCGGTTGTGCTGTGCTCTGAGGCTG 652
Db 433 GTGATGCTTTCTTCTGTGCGGCTGACAGAGAAAGCGGTTGTGCTGTGCTCTGAGGCTG 492
Qy 653 CCGATGCGAGAGAAAGCTGTCTCATCTACATCTCAACCTGTGCGGCGGCGACTTCT 712
Db 493 CCGATGCGAGAGAAAGCTGTCTCATCTACATCTCAACCTGTGCGGCGGCGACTTCT 552
Qy 713 CTTCCTTAGGCGGCACATTAATATGTGCGCGTTAGCGCTCATCAATATCCGCATCCCAT 772
Db 1393 CAGAAATG 1400

Db 553 CTTCCTTAGGCGGCACATTAATATGTGCGCGTTAGCGCTCATCAATATCCGCATCCCAT 612
Qy 773 CTTCAAATCTGATGCTGCTGATGATGATCTTCTCCCTTATATAGGCTTAAGCATGCTGAG 832
Db 613 CTTCAAATCTGATGCTGCTGATGATGATCTTCTCCCTTATATAGGCTTAAGCATGCTGAG 672
Qy 833 CGCCATGAGACCGAGGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 892
Db 673 CGCCATGAGACCGAGGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
Qy 893 CCCAGATACCTGTATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 952
Db 733 CCCAGATACCTGTATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 792
Qy 953 TATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1012
Db 793 TATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 852
Qy 1013 AACGTGATTTCAATTACAAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072
Db 853 AACGTGATTTCAATTACAAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
Qy 1073 CAGCT 1132
Db 913 CAGCT 972
Qy 1133 GTACGTGACCATCTCTCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
Db 973 GTACGTGACCATCTCTCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1032
Qy 1193 TCAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252
Db 1033 TCAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
Qy 1253 TCTAGTTTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1312
Db 1093 TCTAGTTTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1152
Qy 1313 CGTGGGCTCTTTAGGAGGCTCAAAATAGGCAAGCTGAAGCTGTCTCCAGAGGGC 1372
Db 1153 CGTGGGCTCTTTAGGAGGCTCAAAATAGGCAAGCTGAAGCTGTCTCCAGAGGGC 1212
Qy 1373 TCTGACAGACACGCTGAGGTGATGAGGTGAGGGTGTGCTTCTCAGAGAAACCTGGA 1432
Db 1213 TCTGACAGACACGCTGAGGTGATGAGGTGAGGGTGTGCTTCTCAGAGAAACCTGGA 1272
Qy 1433 GCTGTGGGAGAGATTTGAGCAGTGAAGAAAGCTGTGCTGCTGACAGAGACTTT 1492
Db 1273 GCTGTGGGAGAGATTTGAGCAGTGAAGAAAGCTGTGCTGCTGACAGAGACTTT 1332
Qy 1493 GAGAGCAATGCTGCTGCTGCTGACCTTGAACAATTATATGATTTTCTTACCTTGTGCT 1552
Db 1333 GAGAGCAATGCTGCTGCTGCTGACCTTGAACAATTATATGATTTTCTTACCTTGTGCT 1392
Qy 1553 CAGAAATG 1560
Db 1393 CAGAAATG 1400

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Job time : 9593 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 29, 2004, 19:33:38 ; Search time 97 Seconds

(without alignments)
5942.204 Million cell updates/sec

Title: US-09-867-570-1

Sequence: 1 aacaaatgcgcgcgaattcgg.....gaaaaaaaaaaaaaaaaa 2618

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Gapop 60.0 , Gapext 60.0

Searched: 680018 seqs, 110082838 residues

Word size : 20

Total number of hits satisfying chosen parameters: 3851

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending Patents NA New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1088	41.6	1400	US-10-957-135-30	Sequence 30, Appl
2	120	4.6	2040	US-10-957-135-15	Sequence 15, Appl
3	97	3.7	1604	US-10-957-135-32	Sequence 32, Appl
4	46	1.8	1300	US-10-957-135-17	Sequence 17, Appl
5	37	1.4	1979	US-10-957-135-62	Sequence 62, Appl
6	37	1.4	2110	US-10-957-135-58	Sequence 58, Appl
7	37	1.4	2401	US-10-957-135-56	Sequence 56, Appl
8	34	1.3	2093	US-10-957-135-54	Sequence 54, Appl
9	34	1.3	2758	US-10-957-135-72	Sequence 72, Appl
10	33	1.3	1519	US-10-957-135-52	Sequence 52, Appl
11	33	1.3	1738	US-10-957-135-74	Sequence 74, Appl
12	31	1.2	1045	US-10-957-135-24	Sequence 24, Appl
13	31	1.2	1088	US-10-957-135-1	Sequence 1, Appl
14	28	1.1	1010	US-10-220-366A-9630	Sequence 9630, Ap
15	26	1.0	1485	US-10-957-135-64	Sequence 64, Appl
16	25	1.0	395	US-10-220-366A-7081	Sequence 7081, Ap
17	25	1.0	573	US-10-956-160-6514	Sequence 6514, Ap
18	25	1.0	573	US-10-956-160-21621	Sequence 21621, Ap
19	25	1.0	578	US-10-956-160-7449	Sequence 7449, Ap
20	25	1.0	578	US-10-956-160-217556	Sequence 217556, Ap
21	25	1.0	586	US-10-956-160-1226	Sequence 1226, Ap
22	25	1.0	586	US-10-956-160-211333	Sequence 211333, Ap
23	25	1.0	980	US-10-957-135-26	Sequence 26, Appl
24	25	1.0	1024	US-10-957-135-22	Sequence 22, Appl
25	25	1.0	2853	US-10-957-135-11	Sequence 11, Appl

26	25	1.0	4293	US-10-811-028A-2	Sequence 2, Appl
27	25	1.0	4332	US-10-811-028A-1	Sequence 1, Appl
28	24	0.9	368	US-10-220-366A-5762	Sequence 5762, Ap
29	24	0.9	574	US-10-956-160-10950	Sequence 10950, A
30	24	0.9	574	US-10-956-160-221057	Sequence 221057, A
31	24	0.9	697	US-10-956-157-2831	Sequence 2831, Ap
32	24	0.9	697	US-10-956-157-8066	Sequence 8066, Ap
33	24	0.9	90100	PCT-US03-40884-1	Sequence 1, Appl
34	23	0.9	152	US-10-956-160-12217	Sequence 12217, A
35	23	0.9	201	US-10-220-366A-3751	Sequence 3751, Ap
36	23	0.9	240	US-10-956-160-11880	Sequence 11880, A
37	23	0.9	240	US-10-956-157-221987	Sequence 221987, A
38	23	0.9	293	US-10-220-366A-10832	Sequence 10832, A
39	23	0.9	385	US-10-857-294-1	Sequence 1400, Ap
40	23	0.9	394	US-10-220-366A-1400	Sequence 1400, Ap
41	23	0.9	398	US-10-220-366A-2372	Sequence 2372, Ap
42	23	0.9	400	US-10-220-366A-7410	Sequence 7410, Ap
43	23	0.9	403	US-10-220-366A-5577	Sequence 5577, Ap
44	23	0.9	410	US-10-956-160-5873	Sequence 5873, Ap
45	23	0.9	410	US-10-956-160-215980	Sequence 215980, Ap

ALIGNMENTS

RESULT 1
US-10-957-135-30
Sequence 30, Application US/10957135
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhang
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-Kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE, 4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (332)...(1297)
US-10-957-135-30

Query Match 41.6%; Score 1088; DB 6; Length 1400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 473 CAGACTGGGTTCTGAGCATGATTCACATCCAGTCTGGGTACAGAACTGACACC 532
DB 313 CAGACTGGGTTCTGAGCATGATTCACATCCAGTCTGGGTACAGAACTGACACC 372
QY 533 AATCAACGAGCGTGAAGAGACTCTCTTCTCAAGAGAGACCTTGAAGCTTCAACGGGCTGAC 592
DB 373 AATCAACGAGCGTGAAGAGACTCTCTTCTCAAGAGAGACCTTGAAGCTTCAACGGGCTGAC 432


```
QY 593 GTGATGCTTTCCCTTGTGCGGCTGACAGAGAAACGGTTGCTCTGCGCTCTGGCTG 652
| | | | |
Db 433 GTGATGCTTTCCCTTGTGCGGCTGACAGAGAAACGGTTGCTCTGCGCTCTGGCTG 492
| | | | |
QY 653 CCGCATGCGAGAGAACGCTGTCTCATCTACATCTCTAACCTGCTGCGGCTCGCATCTTCT 712
| | | | |
Db 493 CCGCATGCGAGAGAACGCTGTCTCATCTACATCTCTAACCTGCTGCGGCTCGCATCTTCT 552
| | | | |
QY 713 CTTCCTTAGCGGACCATTTATATGTTGCGCGTTAGCGGCTCATCAATATCCGCACTCCAT 772
| | | | |
Db 553 CTTCCTTAGCGGACCATTTATATGTTGCGCGTTAGCGGCTCATCAATATCCGCACTCCAT 612
| | | | |
QY 773 CTCCAAATCTCTCACTCTGTGATGACCTTTCTCTTATATAGGCTTAAGCATGCTGAG 832
| | | | |
Db 613 CTCCAAATCTCTCACTCTGTGATGACCTTTCTCTTATATAGGCTTAAGCATGCTGAG 672
| | | | |
QY 833 CGCATGAGACACGAGCGCTGCTCTCATCTGTGAGCCCATCTGTGACATCTGCGCGCG 892
| | | | |
Db 673 CGCATGAGACACGAGCGCTGCTCTCATCTGTGAGCCCATCTGTGACATCTGCGCGCG 732
| | | | |
QY 893 CCCCAGATACCTGTCATGCTGATGCTGTGCTGCTGCTGCGGCTGCTGCTGCTGCGAG 952
| | | | |
Db 733 CCCCAGATACCTGTCATGCTGATGCTGTGCTGCTGCTGCGGCTGCTGCTGCTGCGAG 792
| | | | |
QY 953 TATCTGTGAGTGTATGTTCTGTGACTTCTGTTAGTGTGCTGATCTGTTGTGTGA 1012
| | | | |
Db 793 TATCTGTGAGTGTATGTTCTGTGACTTCTGTTAGTGTGCTGATCTGTTGTGTGA 852
| | | | |
QY 1013 AACGTCAATTTTCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
| | | | |
Db 853 AACGTCAATTTTCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 912
| | | | |
QY 1073 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1132
| | | | |
Db 913 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
| | | | |
QY 1133 GTACGTGACCAATCTCTCTCAAGTGTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTG 1192
| | | | |
Db 973 GTACGTGACCAATCTCTCTCAAGTGTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTG 1032
| | | | |
QY 1193 TCAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1252
| | | | |
Db 1033 TCAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1092
| | | | |
QY 1253 TCTAGTTTCCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1312
| | | | |
Db 1093 TCTAGTTTCCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1152
| | | | |
QY 1313 CGTGGGCTCTTTTAGGACAGCGTCAAAATAGGAGAACTGAAAGCTGTTCTCAAGAGGC 1372
| | | | |
Db 1153 CGTGGGCTCTTTTAGGACAGCGTCAAAATAGGAGAACTGAAAGCTGTTCTCAAGAGGC 1212
| | | | |
QY 1373 TCTGCAAGACACGCTGAGTGTGAGTGAAGAGTGAAGAGTGGCTTCTCAAGAAACCTGGA 1432
| | | | |
Db 1213 TCTGCAAGACACGCTGAGTGTGAGTGAAGAGTGAAGAGTGGCTTCTCAAGAAACCTGGA 1272
| | | | |
QY 1433 GCTGTGCGGAGACAGATTGAGACAGTGAAGAGAACTCTGCTGCTGCTGCTGCTGCTGCT 1492
| | | | |
Db 1273 GCTGTGCGGAGACAGATTGAGACAGTGAAGAGAACTCTGCTGCTGCTGCTGCTGCTGCT 1332
| | | | |
QY 1493 GAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1552
| | | | |
Db 1333 GAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1392
| | | | |
QY 1553 CAGAAATG 1560
| | | | |
Db 1393 CAGAAATG 1400
| | | | |
```

RESULT 2
US-10-957-135-15
Sequence 15, Application US/10957135
GENERAL INFORMATION:

```
APPLICANT: Anderson, David J.  
APPLICANT: Dong, Xinzong  
APPLICANT: Zylka, Mark  
APPLICANT: Simon, Melvin  
APPLICANT: Han, Sang-kyou  
TITLE OF INVENTION: PAIN SIGNALING MOLECULES  
FILE REFERENCE: CALTE, 4C1CPICT  
CURRENT APPLICATION NUMBER: US/10/957,135  
CURRENT FILING DATE: 2004-09-30  
PRIOR APPLICATION NUMBER: US 60/222,344  
PRIOR FILING DATE: 2000-08-01  
PRIOR APPLICATION NUMBER: US 60/202,027  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 09/704,707  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/285,493  
PRIOR FILING DATE: 2001-04-19  
PRIOR APPLICATION NUMBER: US 09/849,869  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 10/183,116  
PRIOR FILING DATE: 2002-06-26  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 2040  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (328)...(1293)  
US-10-957-135-15  
Query Match 4.6%; Score 120; DB 6; Length 2040;  
Best Local Similarity 100.0%; Pred. No. 3.9e-42;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1263 ATTTCTGCTGCTGCTTCTTAACAGACAGTCCCAACCCCATCTTACTTTGTGGGCTCC 1322
| | | | |
Db 1099 ATTTCTGCTGCTGCTTCTTAACAGACAGTCCCAACCCCATCTTACTTTGTGGGCTCC 1158
| | | | |
QY 1322 TTAGGAGCGCTCAAAATAGGAGAACTGAAGTGTCTTCCAGAGGCTCTGACAGAC 1382
| | | | |
Db 1159 TTAGGAGCGCTCAAAATAGGAGAACTGAAGTGTCTTCCAGAGGCTCTGACAGAC 1218
| | | | |
RESULT 3  
US-10-957-135-32  
Sequence 32, Application US/10957135  
GENERAL INFORMATION:  
APPLICANT: Anderson, David J.  
APPLICANT: Dong, Xinzong  
APPLICANT: Zylka, Mark  
APPLICANT: Simon, Melvin  
APPLICANT: Han, Sang-kyou  
TITLE OF INVENTION: PAIN SIGNALING MOLECULES  
FILE REFERENCE: CALTE, 4C1CPICT  
CURRENT APPLICATION NUMBER: US/10/957,135  
CURRENT FILING DATE: 2004-09-30  
PRIOR APPLICATION NUMBER: US 60/222,344  
PRIOR FILING DATE: 2000-08-01  
PRIOR APPLICATION NUMBER: US 60/202,027  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 09/704,707  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/285,493  
PRIOR FILING DATE: 2001-04-19  
PRIOR APPLICATION NUMBER: US 09/849,869  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 10/183,116  
PRIOR FILING DATE: 2002-06-26  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32
```

LENGTH: 1604
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (433)...(1398)
US-10-957-135-32

Query Match 3.7%; Score 97; DB 6; Length 1604;
Best Local Similarity 100.0%; Pred. No. 2.5e-32;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1287 AGTGCACCCCATCATTTACTTCTGCGGCTCTTATGACGCTCAAAATAGCAG 1346
Db 1228 AGTGCACCCCATCATTTACTTCTGCGGCTCTTATGACGCTCAAAATAGCAG 1287

Qy 1347 AACCTGAGCTGTTCTTCAGAGGCTCTGCAGACA 1383
Db 1288 AACCTGAGCTGTTCTTCAGAGGCTCTGCAGACA 1324

RESULT 4
US-10-957-135-17
Sequence 17, Application US/10957135
GENERAL INFORMATION:

APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CPICT
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17
LENGTH: 1300
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (171)...(1160)
US-10-957-135-17

Query Match 1.8%; Score 46; DB 6; Length 1300;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1276 CTCTTAACAGCAGTGCACCCCATCATTTACTTCTGCGGCTC 1321
Db 976 CTCTTAACAGCAGTGCACCCCATCATTTACTTCTGCGGCTC 1021

RESULT 5
US-10-957-135-62
Sequence 62, Application US/10957135
GENERAL INFORMATION:

APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark

APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CPICT
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 62
LENGTH: 1979
TYPE: DNA
ORGANISM: Mus musculus
US-10-957-135-62

Query Match 1.4%; Score 37; DB 6; Length 1979;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1288 GTGCCAACCACCATTTACTTCTGCGGCTCCTT 1324
Db 961 GTGCCAACCACCATTTACTTCTGCGGCTCCTT 997

RESULT 6
US-10-957-135-58
Sequence 58, Application US/10957135
GENERAL INFORMATION:

APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CPICT
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 58
LENGTH: 2110
TYPE: DNA
ORGANISM: Mus musculus
US-10-957-135-58

Query Match 1.4%; Score 37; DB 6; Length 2110;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1288 GTGCCAACCACCATTTACTTCTGCGGCTCCTT 1324

Db 1087 GTGCCAACCCCATCTTACTTCTTCGTGGGCTCCTT 1123

RESULT 7
US-10-957-135-56/c

; Sequence 56, Application US/10957135
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI1
; CURRENT FILING DATE: US/10/957,135
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 10/183,116
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-957-135-56

Query Match 1.4%; Score 37; DB 6; Length 2401;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1288 GTGCCAACCCCATCTTACTTCTTCGTGGGCTCCTT 1324
DB 1138 GTGCCAACCCCATCTTACTTCTTCGTGGGCTCCTT 1102

RESULT 8
US-10-957-135-54

; Sequence 54, Application US/10957135
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI1
; CURRENT FILING DATE: US/10/957,135
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 10/183,116
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 54
; LENGTH: 2093
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-957-135-54

Query Match 1.3%; Score 34; DB 6; Length 2093;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1288 GTGCCAACCCCATCTTACTTCTTCGTGGGCTC 1321
DB 1371 GTGCCAACCCCATCTTACTTCTTCGTGGGCTC 1404

RESULT 9
US-10-957-135-72/c

; Sequence 72, Application US/10957135
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI1
; CURRENT FILING DATE: US/10/957,135
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 10/183,116
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 2758
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-957-135-72

Query Match 1.3%; Score 34; DB 6; Length 2758;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1288 GTGCCAACCCCATCTTACTTCTTCGTGGGCTC 1321
DB 1121 GTGCCAACCCCATCTTACTTCTTCGTGGGCTC 1088

RESULT 10
US-10-957-135-52

; Sequence 52, Application US/10957135
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhang
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI1
; CURRENT FILING DATE: US/10/957,135
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027

```

; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 10/183,116
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 52
; LENGTH: 1519
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-957-135-52

```

```

Query Match 1.3%; Score 33; DB 6; Length 1519;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1289 TGGCAACCCATCATTTACTTCTTCGTGGGCTC 1321
Db 854 TGGCAACCCATCATTTACTTCTTCGTGGGCTC 886

```

```

RESULT 11
US-10-957-135-74
; Sequence 74, Application US/10957135
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI1
; CURRENT APPLICATION NUMBER: US/10/957,135
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 10/183,116
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 74
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-957-135-74

```

```

Query Match 1.3%; Score 33; DB 6; Length 1738;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1292 CAACCCATCATTTACTTCTTCGTGGGCTCCTT 1324
Db 794 CAACCCATCATTTACTTCTTCGTGGGCTCCTT 826

```

```

RESULT 12
US-10-957-135-24
; Sequence 24, Application US/10957135
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.

```

```

; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI1
; CURRENT APPLICATION NUMBER: US/10/957,135
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 10/183,116
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 24
; LENGTH: 1045
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(1020)
US-10-957-135-24

```

```

Query Match 1.2%; Score 31; DB 6; Length 1045;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1288 GTGGCAACCCATCATTTACTTCTTCGTGGG 1318
Db 872 GTGGCAACCCATCATTTACTTCTTCGTGGG 902

```

```

RESULT 13
US-10-957-135-1
; Sequence 1, Application US/10957135
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI1
; CURRENT APPLICATION NUMBER: US/10/957,135
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 10/183,116
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: CDS

```

LOCATION: (115)... (1026)
US-10-957-135-1

Query Match 1.2%; Score 31; DB 6; Length 1088;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1288 GTGCCAACCCTCATTTACTTCTTCTGCGG 1318
DB 878 GTGCCAACCCTCATTTACTTCTTCTGCGG 908

RESULT 14
US-10-220-366A-9630/c
Sequence 9630, Application US/10220366A

GENERAL INFORMATION:
APPLICANT: HYSEQ, INC
TITLE OR INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042
CURRENT APPLICATION NUMBER: US/10/220,366A
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: Custom
SEQ ID NO 9630
LENGTH: 1010
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)... (1010)
OTHER INFORMATION: n = a,t,c or g
US-10-220-366A-9630

Query Match 1.1%; Score 28; DB 6; Length 1010;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 ATAAATTTCCAGTCTCAGTATTCTT 248
DB 402 ATAAATTTCCAGTCTCAGTATTCTT 375

RESULT 15
US-10-957-135-64
Sequence 64, Application US/10957135

GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhang
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OR INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 64
LENGTH: 1485
TYPE: DNA
ORGANISM: Mus musculus
US-10-957-135-64

Query Match 1.0%; Score 26; DB 6; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1288 GTGCCAACCCTCATTTACTTCTTC 1313
DB 926 GTGCCAACCCTCATTTACTTCTTC 951

Search completed: October 30, 2004, 03:32:11
Job time: 102 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 18:51:18 ; Search time 7918 Seconds
(without alignments)
12048.338 Million cell updates/sec

Title: US-09-867-570-1
Perfect score: 2618
Sequence: 1 aacaaatgcgcgcgaattcgg.....gaaaaaaaaaaaaaaaaa 2618

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapept 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 20

Total number of hits satisfying chosen parameters: 317745

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST.*
1: gb_esc1.*
2: gb_esc2.*
3: gb_esc3.*
4: gb_esc4.*
5: gb_esc5.*
6: gb_esc6.*
7: gb_esc7.*
8: gb_esc8.*
9: gb_esc9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	21.0	889	6 CA455045	AGENCOURT
2	530	20.2	688	2 BR439409	HTM1-025F
3	313	12.0	662	1 AV731610	AV731610
4	269	10.3	905	6 CD243595	AGENCOURT
5	120	4.6	764	4 BG198766	RST18035
6	120	4.6	1009	7 CN837763	AGENCOURT
7	115	4.4	871	4 BG210740	RST30287
8	97	3.7	827	7 CN831885	AGENCOURT
9	97	3.7	825	7 CN843633	AGENCOURT
10	97	3.7	863	7 CN835944	AGENCOURT
11	97	3.7	895	7 CN840024	AGENCOURT
12	97	3.7	924	7 CN839634	AGENCOURT
13	97	3.7	953	7 CN839765	AGENCOURT
14	89	3.4	184	4 BG195197	RST14376
15	85	3.2	248	4 BG196705	RST15931
16	82	3.1	515	1 AL705589	DKFZP686K
17	81	3.1	552	8 AQ392205	KITB1-E1-
18	69	2.6	825	7 CN843258	AGENCOURT
19	67	2.6	1207	7 CN831816	AGENCOURT
20	57	2.2	924	6 CD051096	AGENCOURT
21	46	1.8	503	1 AF003828	AF003828
22	44	1.7	468	8 B74348	CIT-HSP-204
23	44	1.7	825	7 CN835770	AGENCOURT
24	44	1.7	826	7 CN839711	AGENCOURT

25	44	1.7	835	7 CN834097	CN834097
26	44	1.7	851	7 CN839827	CN839827
27	44	1.7	899	7 CN843534	CN843534
28	43	1.6	419	1 AL118979	AL118979
29	43	1.6	855	7 CN839609	CN839609
30	41	1.6	435	8 AQ192307	AQ192307
31	41	1.6	811	7 CN831931	CN831931
32	41	1.6	871	7 CN839125	CN839125
33	41	1.6	954	7 CN842891	CN842891
34	40	1.5	630	8 AQ696198	AQ696198
35	39	1.5	618	8 AQ587244	AQ587244
36	39	1.5	1114	7 CN837998	CN837998
37	38	1.5	636	9 AG013749	AG013749
38	38	1.5	692	9 AG013779	AG013779
39	38	1.5	694	9 AG013746	AG013746
40	38	1.5	698	9 AG013748	AG013748
41	38	1.5	787	4 BG208126	BG208126
42	37	1.4	503	8 AQ888076	AQ888076
43	36	1.4	191	7 T59759	T59759
44	36	1.4	598	8 AQ583508	AQ583508
45	35	1.3	141	7 H49498	H49498

ALIGNMENTS

RESULT 1
CA455045
LOCUS
DEFINITION
AGENCOURT_10735784 MABCL Homo sapiens CDNA clone IMAGE:6722551 5', mRNA sequence.
ACCESSION
CA455045
VERSION
CA455045.1 GI:24905369
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM4285 Row: h Column: 07
High quality sequence stop: 743.
Location/Qualifiers
1. 889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6722551"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, HTERT-HME1, LNCaP"
/lab_host="EMDH1.0B"
/clone_id="MABCL"
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subcloned with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strauberg, Bungkok Lee & Ira Pastan. Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

FEATURES

ORIGIN

Query Match 21.0%; Score 550; DB 6; Length 889;
Best Local Similarity 99.6%; Pred. No. 3.7e-267;
Matches 700; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY GGGTCATCAGACTGGGGTTTCTGACATGAGATTCAACCATCCAGCTTGGGTACAGAAC 525
DB GGGTCATCAGACTGGGGTTTCTGACATGAGATTCAACCATCCAGCTTGGGTACAGAAC 206
QY TGAACCAATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
DB TGAACCAATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 266
QY GGTGACGTCGATCGTTTCCCTTGTGCGCTGACAGAGAAACGGTGTGCTGCGCTCC 645
DB GGTGACGTCGATCGTTTCCCTTGTGCGCTGACAGAGAAACGGTGTGCTGCGCTCC 326
QY TGGGCTGCGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
DB TGGGCTGCGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 386
QY ACTTCCTTCTTCCTTTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
DB ACTTCCTTCTTCCTTTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446
QY ATCCCATCTCCAAATCTCAGTCTGATGATGATGATGATGATGATGATGATGATGATG 825
DB ATCCCATCTCCAAATCTCAGTCTGATGATGATGATGATGATGATGATGATGATGATG 506
QY TGTGAGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
DB TGTGAGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
QY TGTGAGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
DB TGTGAGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
QY GCGCGCGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 945
DB GCGCGCGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 626
QY TGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1005
DB TGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 686
QY GGTGTGAACGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065
DB GGTGTGAACGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 746
QY GTGGGTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1125
DB GTGGGTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 806
QY TGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1168
DB TGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
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RESULT 2
BE439409 688 bp mRNA linear EST 25-JUL-2000
LOCUS BE439409
DEFINITION HTM1-025F1 HTM1 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE439409
VERSION BE439409.1 GI:9438891
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 688)
AUTHORS Gonzalez, P., Epstein, D.L. and Borras, T.
TITLE Characterization of gene expression in human trabecular meshwork
JOURNAL using single-pass sequencing of 1060 clones
COMMENT Contact: Pedro Gonzalez
Department of Ophthalmology
Duke University
Duke Eye Center, Erwin Rd, Box 3802, Durham, NC 27710-3802, USA

Tel: 919 681 4085
Fax: 919 684 8983
Email: pedro.gonzalez@duke.edu.
Location/Qualifiers

FEATURES
source 1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cbase_type="Trabecular meshwork"
/clone_lib="HTM1"

ORIGIN

Query Match 20.2%; Score 530; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 5.3e-257;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY GGGTCATCAGACTGGGGTTTCTGACATGAGATTCAACCATCCAGCTTGGGTACAGAAC 525
DB GGGTCATCAGACTGGGGTTTCTGACATGAGATTCAACCATCCAGCTTGGGTACAGAAC 93
QY TGAACCAATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
DB TGAACCAATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 153
QY GGTGACGTCGATCGTTTCCCTTGTGCGCTGACAGAGAAACGGTGTGCTGCGCTCC 645
DB GGTGACGTCGATCGTTTCCCTTGTGCGCTGACAGAGAAACGGTGTGCTGCGCTCC 213
QY TGGGCTGCGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
DB TGGGCTGCGGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 273
QY ACTTCCTTCTTCCTTTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
DB ACTTCCTTCTTCCTTTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 333
QY ATCCCATCTCCAAATCTCAGTCTGATGATGATGATGATGATGATGATGATGATGATG 825
DB ATCCCATCTCCAAATCTCAGTCTGATGATGATGATGATGATGATGATGATGATGATG 393
QY TGTGAGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
DB TGTGAGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 453
QY TGTGAGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
DB TGTGAGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 513
QY GCGCGCGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 945
DB GCGCGCGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 513
QY TGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 995
DB TGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 563
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RESULT 3
AV731610 662 bp mRNA linear EST 17-OCT-2000
LOCUS AV731610
DEFINITION HTF Homo sapiens cDNA clone HTFAXD08 5', mRNA sequence.
ACCESSION AV731610
VERSION AV731610.1 GI:10849155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 662)
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
TITLE Homo sapiens cDNA HTF clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

FEATURES

source
1..662
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HTFAD08"
/cissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1ib="HTF"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 12.0%; Score 313; DB 1; Length 662;

Best Local Similarity 99.4%; Pred. No. 8e-147; Mismatches 3; Indels 0; Gaps 0;

Matches 463; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1591 ATGTTATCTTAACTGAGTGGAGTGGTTCACCAAGAAAGATTAGTCTGACAGTAC 1650

32 ATGTTATCTTAACTGAGTGGAGTGGTTCACCAAGAAAGATTAGTCTGACAGTAC 91

1651 AATGTTGAGTCTCTTGAATATTAACCAATATTTCCCTGTTATCTTCACTGAATCT 1710

92 AATGTTGAGTCTCTTGAATATTAACCAATATTTCCCTGTTATCTTCACTGAATCT 151

1711 TTCTCTAGTGAACCTTTTCTGCACTTTTCACTGTAATATAAGAGTCTGTCACAC 1770

152 TTCTCTAGTGAACCTTTTCTGCACTTTTCACTGTAATATAAGAGTCTGTCACAC 211

1771 CCTAAAGCTCTTCTTATACCTGTTCTCTGCTAGTATCAAAAAGAAAGATTCTTA 1830

212 CCTAAAGCTCTTCTTATACCTGTTCTCTGCTAGTATCAAAAAGAAAGATTCTTA 271

1831 TTAATCTGTCAGTATGTTCCCTGAAATATCATGTTCCCTTTATGATGAGGCACTTA 1890

272 TTAATCTGTCAGTATGTTCCCTGAAATATCATGTTCCCTTTATGATGAGGCACTTA 331

1891 CTGCAAGTGGAGCTCAATCTTATATAGAGTGTCTGCTAAGCTTAATTCATTGAAT 1950

332 CTGCAAGTGGAGCTCAATCTTATATAGAGTGTCTGCTAAGCTTAATTCATTGAAT 391

1951 TCTCAGATTAAGCAAAATATGAGCTTATGAGAGAGATTCTCCCTCATTAAGAGTCT 2010

392 TCTCAGATTAAGCAAAATATGAGCTTATGAGAGAGATTCTCCCTCATTAAGAGTCT 451

2011 TTAGAAATTGGTTTATGAAATAGCCCTCTCTGTCATTGTCACA 2056

452 TTAGAAATTGGTTTATGAAATAGCCCTCTCTGTCATTGTCACA 497

2056

CD243595 905 bp mRNA linear EST 22-MAY-2003

AGENCY: 1412113 NIH MGC 180 Homo sapiens cDNA clone

IMAG: 30383708 5', mRNA sequence.

CD243595 CD243595.1 GI:31004059

EST.
Homo sapiens (human)
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaaps-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

plate: NDMA47 row: p column: 21

High quality sequence start: 20

High quality sequence stop: 592.

Location/Qualifiers

FEATURES

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAG:30383708"
/lab_host="DH10B-Ton A (T1 and T5 phage resistance)"
/note="Organ: Testis; Vector: pCMV-Sport6.1; Site 1: NotI;
Site 2: EcoRV (destroyed); Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.68 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 10.3%; Score 269; DB 6; Length 905;

Best Local Similarity 100.0%; Pred. No. 1.8e-124; Mismatches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

466 GGGTCATCAACAGCGGGTTTCTGAGCATGATTCACCAATCCAGTCTGGGTACAGAC 525

364 GGGTCATCAACAGCGGGTTTCTGAGCATGATTCACCAATCCAGTCTGGGTACAGAC 423

526 TGACCAATCAACAGCGGTGAGAGAGCTCTTCTCAAGAGAGCCCTGAGCTTCAAG 585

424 TGACCAATCAACAGCGGTGAGAGAGCTCTTCTCAAGAGAGCCCTGAGCTTCAAG 483

586 GGGTCATCAACAGCGGGTTTCTGAGCATGATTCACCAATCCAGTCTGGGTACAGAC 645

484 GGGTCATCAACAGCGGGTTTCTGAGCATGATTCACCAATCCAGTCTGGGTACAGAC 543

646 TGGGTCGCCGAGAGAGAGAGAGAGCTCTTCTCAAGAGAGCCCTGAGCTTCAAG 705

544 TGGGTCGCCGAGAGAGAGAGAGAGCTCTTCTCAAGAGAGCCCTGAGCTTCAAG 603

706 ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

604 ACTTCTCTCTCTTGAAGGCGGCACTTATA 632

734

ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

632

ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

734

ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

734

ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

FEATURES

source
1..905
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAG:30383708"
/lab_host="DH10B-Ton A (T1 and T5 phage resistance)"
/note="Organ: Testis; Vector: pCMV-Sport6.1; Site 1: NotI;
Site 2: EcoRV (destroyed); Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.68 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 10.3%; Score 269; DB 6; Length 905;

Best Local Similarity 100.0%; Pred. No. 1.8e-124; Mismatches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

466 GGGTCATCAACAGCGGGTTTCTGAGCATGATTCACCAATCCAGTCTGGGTACAGAC 525

364 GGGTCATCAACAGCGGGTTTCTGAGCATGATTCACCAATCCAGTCTGGGTACAGAC 423

526 TGACCAATCAACAGCGGTGAGAGAGCTCTTCTCAAGAGAGCCCTGAGCTTCAAG 585

424 TGACCAATCAACAGCGGTGAGAGAGCTCTTCTCAAGAGAGCCCTGAGCTTCAAG 483

586 GGGTCATCAACAGCGGGTTTCTGAGCATGATTCACCAATCCAGTCTGGGTACAGAC 645

484 GGGTCATCAACAGCGGGTTTCTGAGCATGATTCACCAATCCAGTCTGGGTACAGAC 543

646 TGGGTCGCCGAGAGAGAGAGAGAGCTCTTCTCAAGAGAGCCCTGAGCTTCAAG 705

544 TGGGTCGCCGAGAGAGAGAGAGAGCTCTTCTCAAGAGAGCCCTGAGCTTCAAG 603

706 ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

604 ACTTCTCTCTCTTGAAGGCGGCACTTATA 632

734

ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

632

ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

734

ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

734

ACTTCTCTCTCTTGAAGGCGGCACTTATA 734

MEDLINE
21227151
PUBMED
11329013
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 559.
Location/Qualifiers
1..764
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 4.6%; Score 120; DB 4; Length 764;
Best Local Similarity 100.0%; Pred. No. 7.9e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1263 ATTTTCCTGTCGCTTTAAGCAGAGTGCCACCCCATTTACTTCTTCGTGGGCTCC 1322
|||||
DB 177 ATTTTCCTGTCGCTTTAAGCAGAGTGCCACCCCATTTACTTCTTCGTGGGCTCC 118
|||||

QY 1323 TTTAGGCAAGCTTCATAATAGGAGAACCTGAAGCTGTTCTCAGAGGGCTCTGCAGGAC 1382
|||||
DB 117 TTTAGGCAAGCTTCATAATAGGAGAACCTGAAGCTGTTCTCAGAGGGCTCTGCAGGAC 58
|||||

RESULT 6
CN837763/c 1009 bp mRNA linear EST 02-JUN-2004
LOCUS
AGENCOURT 15864212 NIH MGC 145 Homo sapiens cDNA clone
IMAGE:30706611 3', mRNA sequence.
ACCESSION
CN837763
VERSION
CN837763.1 GI:47943418
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1009)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@nci.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LINT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINT at:
<http://image.llnl.gov>
Plate: IRB14 row: e column: 04
High quality sequence stop: 464.
Location/Qualifiers
1..1009
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30706611"

FEATURES
source

/tissue_type="mixed"
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/clone_lib="NIH MGC 145"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XbaI/XhoI-3', 5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 4.6%; Score 120; DB 7; Length 1009;
Best Local Similarity 100.0%; Pred. No. 7.9e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1263 ATTTTCCTGTCGCTTTAAGCAGAGTGCCACCCCATTTACTTCTTCGTGGGCTCC 1322
|||||
DB 236 ATTTTCCTGTCGCTTTAAGCAGAGTGCCACCCCATTTACTTCTTCGTGGGCTCC 177
|||||

QY 1323 TTTAGGCAAGCTTCATAATAGGAGAACCTGAAGCTGTTCTCAGAGGGCTCTGCAGGAC 1382
|||||
DB 176 TTTAGGCAAGCTTCATAATAGGAGAACCTGAAGCTGTTCTCAGAGGGCTCTGCAGGAC 117
|||||

RESULT 7
BG210740/c 871 bp mRNA linear EST 21-APR-2001
LOCUS
RST30287 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG210740
VERSION
BG210740.1 GI:13732427
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 871)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,
Mays, R., Smith, B., Veloso, N., Kilka, A., Hess, J., Cottrien, K., Lo, K.,
Offendackner, J., Danzig, J. and Ducart, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
MEDLINE
21227151
PUBMED
11329013
COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 456.
Location/Qualifiers
1..871
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 4.4%; Score 115; DB 4; Length 871;
Best Local Similarity 100.0%; Pred. No. 2.7e-46;

	Matches	115,	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1268	CCTGTCCGCTCTTAAACAGCAGTGGCAACCCATCATATTACTTTCTTCGTGGGCTCCTTAG	1327							
Db	158	CGTCTCCGCTCTTAAACAGCAGTGGCAACCCATCATATTACTTTCTTCGTGGGCTCCTTAG	99							
Oy	1328	GCAGCGCAAAATAATGGAGAACCTGAAGCTGTTCTCCAGAGGGCTCGCAGGAC	1382							
Db	98	GCAGCGCAAAATAATGGAGAACCTGAAGCTGTTCTCCAGAGGGCTCGCAGGAC	44							
	RESULT 8									
	CN831885/c									
	LOCUS									
	DEFINITION	CN831885	827 bp	mRNA	linear	EST 02-JUN-2004				
	IMAGE:	AGENCOURT_15669850 NIH_MGC_145 Homo sapiens cDNA clone								
	IMAGE:	30706617 5', mRNA sequence.								
	CN831885									
	KEYWORDS	CN831885.1 GI:47935638								
	SOURCE	EST.								
	ORGANISM	Homo sapiens (human)								
	AUTHORS	Homo sapiens								
	TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.								
	COMMENT	NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-re@mail.nih.gov Tissue Procurement: GPCR Consortium CDNA Library Preparation: GPCR Consortium CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: IRB14 row: e column: 10 High quality sequence stop: 653. Location/Qualifiers								
	FEATURES									
	source	1..827								
		/organism="Homo sapiens"								
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		/clone="IMAGE:30706617"								
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		/clone_idb="NIH_MGC_145"								
		/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-ScorV-XmnI/XhoI-3', 5'-ScorV-XmnI/NotI-3', ScorV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.lnl.gov/image/rearrayed_plates/IRB1.presv.dat a Note: this is a NIH_MGC library."								
	ORIGIN									
	Query Match	3.7%; Score 97;	DB 7;	Length 827;						
	Best Local Similarity	100.0%;	Pred. No. 3.8e-37;							
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Oy	1287	AGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTAGGCAAGCGTCAAAATAGCGAG	1346							
Db	237	AGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTAGGCAAGCGTCAAAATAGCGAG	178							
Oy	1347	AACCTGAAGCTGTCTTCAGAGGGCTCGCAGGACA	1383							
Db	177	AACCTGAAGCTGTCTTCAGAGGGCTCGCAGGACA	141							

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RESULT 9
CN843633/c 835 bp mRNA linear EST 02-JUN-2004
LOCUS
DEFINITION
AGENCOURT15658848 NIH_MGC_145 Homo sapiens cDNA clone
CN843633
IMAGE:30706619 5', mRNA sequence.
ACCESSION
CN843633
VERSION
CN843633.1 GI:47949288
KEYWORDS
EST.
ORGANISM
Homo sapiens (human)
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE
NIH-MGC http://mgs.nci.nih.gov/.
REFERENCE
1 (bases 1 to 835)
NATIONAL INSTITUTE OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: IRB14 row: e column: 12
High quality sequence stop: 660.
Location/Qualifiers
1. 835
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30706619"
/tissue_type="mixed"
/lab host="DH10B"
/clone_lid="NIH_MGC_145"
/notes="vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/Image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

```

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 863)
NHL-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bldg31.nih.gov

Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

Plate: IRB14 row: e column: 11
High quality sequence stop: 719.

FEATURES

source

Location/Qualifiers

1..863

/organism="Homo sapiens"

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/clone_id="NHL-MGC_145"

/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-Xmi/NotI-3',
5'-EcoRV-Xmi/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 3.7%; Score 97; DB 7; Length 863;

Best Local Similarity 100.0%; Pred. No. 3.8e-37;

Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1287 AGTGCACACCCATCTTCTCTGCGGCTCTTACGACGCTCAAAATAGGCG 1346

DB 237 AGTGCACACCCATCTTCTCTGCGGCTCTTACGACGCTCAAAATAGGCG 178

QY 1347 AACCTGAAGCTGTTCTCCAGAGGGCTCTGCAGACA 1383

DB 177 AACCTGAAGCTGTTCTCCAGAGGGCTCTGCAGACA 141

RESULT 11

CN840024/C 895 bp mRNA linear EST 02-JUN-2004

LOCUS AGNCOURT 15864276 NIH_MGC_145 Homo sapiens cDNA clone

DEFINITION IMAGE:30706615 3', mRNA sequence.

ACCESSION CN840024

VERSION CN840024.1 GI:47945679

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 895)

NHL-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cga@bldg31.nih.gov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: IRB14 row: e column: 08

High quality sequence stop: 449.

FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

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/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-Xmi/NotI-3',
5'-EcoRV-Xmi/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 3.7%; Score 97; DB 7; Length 895;

Best Local Similarity 100.0%; Pred. No. 3.8e-37;

Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1287 AGTGCACACCCATCTTCTCTGCGGCTCTTACGACGCTCAAAATAGGCG 1346

DB 236 AGTGCACACCCATCTTCTCTGCGGCTCTTACGACGCTCAAAATAGGCG 197

QY 1347 AACCTGAAGCTGTTCTCCAGAGGGCTCTGCAGACA 1383

DB 196 AACCTGAAGCTGTTCTCCAGAGGGCTCTGCAGACA 160

RESULT 12

CN839634/C

LOCUS AGNCOURT 15864260 NIH_MGC_145 Homo sapiens cDNA clone

DEFINITION IMAGE:30706614 3', mRNA sequence.

ACCESSION CN839634

VERSION CN839634.1 GI:47945289

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 924)

NHL-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cga@bldg31.nih.gov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

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Location/Qualifiers
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/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearranged_plates/IRBI.presv.dat
A Note: this is a NIH_MGC Library."

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.8e-37;
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DB 256 AGTGCACCCCATCTTACTCTTCGTGGGCTCCTTAGGAGGCTCAAAATAGGCAG 197
QY 1347 AACCTGAAGCTGTTCTCCAGAGGGCTCTGCAGAGCA 1383
DB 196 AACCTGAAGCTGTTCTCCAGAGGGCTCTGCAGAGCA 160

RESULT 13
LOCUS CN839765/c 953 bp mRNA linear EST 02-JUN-2004
DEFINITION IMAGE:30706616 3', mRNA sequence.
ACCESSION CN839765
VERSION CN839765.1 GI:47945420
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 953)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: c9abbs@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
High quality sequence stop: 578.
Location/Qualifiers
1..953

FEATURES

source
/organism="Homo sapiens"
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/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearranged_plates/IRBI.presv.dat
A Note: this is a NIH_MGC Library."

ORIGIN

Query Match 3.7%; Score 97; DB 7; Length 953;
Best Local Similarity 100.0%; Pred. No. 3.8e-37;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1287 AGTGCACCCCATCTTACTCTTCGTGGGCTCCTTAGGAGGCTCAAAATAGGCAG 1346
DB 256 AGTGCACCCCATCTTACTCTTCGTGGGCTCCTTAGGAGGCTCAAAATAGGCAG 197
QY 1347 AACCTGAAGCTGTTCTCCAGAGGGCTCTGCAGAGCA 1383
DB 196 AACCTGAAGCTGTTCTCCAGAGGGCTCTGCAGAGCA 160

RESULT 14
LOCUS BG195197/c 184 bp mRNA linear EST 21-APR-2001
DEFINITION RST14376 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG195197
VERSION BG195197.1 GI:13716884
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 184)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lermer, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klike, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL 21227151
MEDLINE 11329013
PUBMED
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 134.
Location/Qualifiers
1..184

FEATURES

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cdl_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 3.4%; Score 89; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.2e-33;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1294 ACCCATCATTTACTCTTCGTGGGCTCCTTAGGAGGCTCAAAATAGGCAACTGA 1353

Db 145 ACCCCATCATTTACTTCTTCTGGGCTCTTTAGGACGCTCAAAATAGGACGAACCTGA 86
 QY 1354 AGCTGTTTCCAGAGGGCTCTGCAGGAC 1382
 Db 85 AGCTGTTTCTCCAGAGGGCTCTGCAGGAC 57

RESULT 15

LOCUS BG196705/c 248 bp mRNA linear EST 21-APR-2001
 DEFINITION RST15931 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG196705
 VERSION BG196705.1 GI:13718392

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,
 Whitington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
 Mays,R., Smith,E., Veloso,N., Kikka,A., Hess,J., Cothren,K., Lo,K.,
 Offenbacher,J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression

TITLE

Creation of genome-wide protein expression libraries using random
 activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL

21227151

MEDLINE

PUBMED

COMMENT

Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596

Email: scain@athersys.com

High quality sequence stop: 198.

Location/Qualifiers

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HT1080"
 /clone_lib="Athersys RAGE Library"
 /note="See 'Creation of Genome-wide Protein Expression'
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 3.2%; Score 85; DB 4; Length 248;
 Best Local Similarity 100.0%; Pred. No. 4.5e-31;

Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1263 ATTTTCGTCGGCTCTTAAGCAGAGTGCAACCCCATCATTTACTTCTTGGGAGCTCC 1322

Db 175 ATTTTCCTGTCGGCTCTTAAGCAGAGTGCAACCCCATCATTTACTTCTTGGGAGCTCC 116

QY 1323 TTAGGACGCGTCAAAATAGGACGA 1347

Db 115 TTAGGACGCGTCAAAATAGGACGA 91

Search completed: October 30, 2004, 00:46:40
 Job time : 7932 secs